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OM protein - protein search, using sw model

Run on: August 28, 2003, 18:02:01 ; Search time 18 Seconds
(without alignments)
669.922 Million cell updates/sec

Title: US-09-507-968D-2
Perfect score: 1451
Sequence: 1 MDDSTEREQSLTSCCLKRE.....ENQAISLDGVTFFGALKLL 285

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_patents_AA.*
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2: /cgn2_6/ptodata/1/iaa/5B.COMB.pap.*
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6: /cgn2_6/ptodata/1/iaa/backfilesi.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1451	100.0	285	3	US-09-286-529-1
2	1451	100.0	285	4	US-09-589-287B-2
3	1451	100.0	285	4	US-09-496-118B-1
4	1451	100.0	285	4	US-09-565-423-2
5	1451	100.0	285	4	US-09-879-919-23
6	1451	100.0	285	4	US-09-588-947A-2
7	1335.5	92.0	266	4	US-09-589-287B-19
8	1335.5	92.0	266	4	US-09-879-919-24
9	1335.5	92.0	266	4	US-09-588-947A-19
10	1080	74.4	219	4	US-09-589-287B-28
11	1080	74.4	219	4	US-09-588-947A-28
12	1074	74.0	219	4	US-09-589-287B-30
13	1074	74.0	219	4	US-09-588-947A-30
14	901	62.1	174	4	US-09-496-118B-5
15	793	54.7	289	4	US-09-589-287B-38
16	793	54.7	289	4	US-09-588-947A-38
17	749	51.6	145	3	US-09-286-529-21
18	579	39.9	155	4	US-09-589-287B-23
19	579	39.9	155	4	US-09-588-947A-23
20	244.5	16.9	250	3	US-08-883-086-2
21	244.5	16.9	250	3	US-09-565-423-3
22	243.5	16.8	233	4	US-10-082-260-2
23	243.5	16.8	233	4	US-08-815-783-2
24	243.5	16.8	233	4	US-09-879-919-2
25	243.5	16.8	250	3	US-09-153-927-4
26	243.5	16.8	250	4	US-09-879-919-11
27	236.5	16.3	234	4	US-09-157-864-2

28	236.5	16.3	247	4	US-09-157-864-4	Sequence 4, Appli
29	235.5	16.2	234	4	US-09-879-919-13	Sequence 13, Appli
30	231	15.9	46	4	US-09-496-118B-2	Sequence 2, Appli
31	229.5	15.8	205	3	US-09-286-529-5	Sequence 5, Appli
32	221.5	15.3	168	4	US-10-082-260-4	Sequence 4, Appli
33	221.5	15.3	168	4	US-08-815-783-4	Sequence 4, Appli
34	221.5	15.3	168	4	US-09-879-919-4	Sequence 4, Appli
35	213.5	14.7	147	3	US-08-883-086-3	Sequence 3, Appli
36	210	14.5	136	4	US-09-589-287B-20	Sequence 20, Appli
37	210	14.5	136	4	US-09-588-947A-20	Sequence 20, Appli
38	172	11.9	34	4	US-09-496-118B-4	Sequence 4, Appli
39	147	10.1	31	4	US-09-496-118B-3	Sequence 3, Appli
40	109.5	7.5	235	3	US-08-883-086-7	Sequence 7, Appli
41	104.5	7.2	163	1	US-07-994-469A-64	Sequence 64, Appli
42	102.5	7.1	391	4	US-09-342-681C-2	Sequence 2, Appli
43	102	7.0	204	4	US-08-815-783-6	Sequence 6, Appli
44	101.5	7.0	155	1	US-07-994-469A-67	Sequence 67, Appli
45	101.5	7.0	155	1	US-07-994-469A-68	Sequence 68, Appli

ALIGNMENTS

RESULT 1

US-09-286-529-1
; Sequence 1, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catharine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 285
; TYPE: PRT
; ORGANISM: human
US-09-286-529-1

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Best Local Similarity 100.0%; Pred. No. 7e-160;
.Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC	60
QY	61	LTWVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPAGAGAPAVTAGLKIFPEPPAP	120
Db	61	LTWVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPAGAGAPAVTAGLKIFPEPPAP	120
QY	121	GGNSQNSRNRKRAVQGPETVTQCLQIADSEPTTOKGYSYTFVPMWLLSFKRGSAL	180
Db	121	GGNSQNSRNRKRAVQGPETVTQCLQIADSEPTTOKGYSYTFVPMWLLSFKRGSAL	180
QY	181	KENKILVKETGYFFIYGVLYTDKTYAMGHLLQKRVHVGDELSTVLFRCIQNPETL	240
Db	181	KENKILVKETGYFFIYGVLYTDKTYAMGHLLQKRVHVGDELSTVLFRCIQNPETL	240
QY	241	PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVTFFGALKLL	285
Db	241	PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVTFFGALKLL	285

RESULT 2

US-09-589-287B-2
; Sequence 2, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokine-alpha

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; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION DATA REMOVED - CHECK PALM OR FILE WRAPPER
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 285
; TYPE: PRT
; ORGANISM: human
US-09-589-287B-2

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Query Match      100.0%; Score 1451; DB 4; Length 285;
Best Local Similarity 100.0%; Pred. No. 7e-160;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 LTWVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
DB 61 LTWVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
QY 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALAE 180
DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALAE 180
QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFLRCIQNNPETL 240
DB 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFLRCIQNNPETL 240
QY 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285
DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285

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RESULT 3
US-09-496-118B-1
; Sequence 1, Application US/09496118B
; Patent No. 6475986
; GENERAL INFORMATION:
; APPLICANT: Aggarwal, Bharat B.
; TITLE OF INVENTION: Uses of THANK, a TNF homologue that Activates
; FILE OF INVENTION: Apoptosis
; FILE REFERENCE: D6206
; CURRENT APPLICATION NUMBER: US/09/496,118B
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: US 60/118,531
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO 1
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: amino acid sequence of THANK protein
US-09-496-118B-1

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Query Match      100.0%; Score 1451; DB 4; Length 285;
Best Local Similarity 100.0%; Pred. No. 7e-160;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MDDSTEREQSRLTSLCKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
QY 61 LTWVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
DB 61 LTWVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
QY 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALAE 180
DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALAE 180

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Db 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALAE 180
QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFLRCIQNNPETL 240
DB 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFLRCIQNNPETL 240
QY 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285
DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285

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RESULT 4
US-09-565-423-2
; Sequence 2, Application US/09565423
; Patent No. 6475987
; GENERAL INFORMATION:
; APPLICANT: Shu, Hong-Bing
; TITLE OF INVENTION: TALL-1 NUCLEIC ACID MOLECULES, PROTEINS, RECEPTORS AND
; FILE OF INVENTION: METHODS OF USE THEREOF
; FILE REFERENCE: 2879-72
; CURRENT APPLICATION NUMBER: US/09/565,423
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: UNKNOWN
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/132,892
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: primer
US-09-565-423-2

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Query Match      100.0%; Score 1451; DB 4; Length 285;
Best Local Similarity 100.0%; Pred. No. 7e-160;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MDDSTEREQSRLTSLCKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
QY 61 LTWVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
DB 61 LTWVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
QY 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALAE 180
DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALAE 180
QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFLRCIQNNPETL 240
DB 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFLRCIQNNPETL 240
QY 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285
DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285

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RESULT 5
US-09-879-919-23
; Sequence 23, Application US/09879919
; Patent No. 6541224
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25

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; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-23

Query Match 100.0%; Score 1451; DB 4; Length 285;
Best Local Similarity 100.0%; Pred. No. 7e-160;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MDDSTERQSLTCLKKREMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60

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DB 61 LTVVSFYQVAALQGDLSRAELQGHHAELPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120

QY 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKSYTFVPWLLSFKRGSALEE 180
DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKSYTFVPWLLSFKRGSALEE 180

QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFQDELSLTLFRCIQNMPEL 240
DB 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFQDELSLTLFRCIQNMPEL 240

QY 241 PNNCSYAGIAKLEEGDELQALIPRENAQISLDGDVTFFGALKLL 285
DB 241 PNNCSYAGIAKLEEGDELQALIPRENAQISLDGDVTFFGALKLL 285

RESULT 6

US-09-588-947A-2
; Sequence 2, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C2
; CURRENT APPLICATION NUMBER: US/09/588,947A
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/588,947
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/507,968
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/122,388
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,097
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/127,598
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/130,412
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/130,696
; PRIOR FILING DATE: 1999-04-23

; PRIOR APPLICATION NUMBER: 60/131,278
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131,673
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/136,784
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/142,659
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: 60/145,824
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: 60/167,239
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 60/168,624
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/171,108
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/171,626
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/176,015
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/255,794
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 09/005,874
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/036,100
; PRIOR FILING DATE: 1997-01-14
; PRIOR APPLICATION NUMBER: PCT/US96/17957
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 285
; TYPE: PRT
; ORGANISM: human
US-09-588-947A-2

Query Match 100.0%; Score 1451; DB 4; Length 285;
Best Local Similarity 100.0%; Pred. No. 7e-160;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 LTVVSFYQVAALQGDLSRAELQGHHAELPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120

QY 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKSYTFVPWLLSFKRGSALEE 180
DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKSYTFVPWLLSFKRGSALEE 180

QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFQDELSLTLFRCIQNMPEL 240
DB 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFQDELSLTLFRCIQNMPEL 240

QY 241 PNNCSYAGIAKLEEGDELQALIPRENAQISLDGDVTFFGALKLL 285
DB 241 PNNCSYAGIAKLEEGDELQALIPRENAQISLDGDVTFFGALKLL 285

RESULT 7

US-09-589-287B-19
; Sequence 19, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-19

Query Match      92.0%; Score 1335.5; DB 4; Length 266;
Best Local Similarity 93.3%; Pred. No. 1.6e-146;
Matches 266; Conservative 0; Mismatches 0; Indels 19; Gaps 1;

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Db 1 MDDSTEREQSLTSCLLKKEEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
QY 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
Db 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
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Db 121 GEGNSSQNSRNKRAVQGPET-----GSYTFVPWLLSFKRGSAL EE 161
QY 181 KENKILVKETGYFFIYGOVLYTDKTYAMGHLIQRKKVHVFGDELSLVTILFRCIQNMPE TL 240
Db 162 KENKILVKETGYFFIYGOVLYTDKTYAMGHLIQRKKVHVFGDELSLVTILFRCIQNMPE TL 221
QY 241 PNNCSYSAGIAKLEEGDELQLAIPRENAQISLDGSDVTFFGALKLL 285
Db 222 PNNCSYSAGIAKLEEGDELQLAIPRENAQISLDGSDVTFFGALKLL 266

RESULT 9
US-09-588-947A-19
; Sequence 19, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P32
; CURRENT APPLICATION NUMBER: US/09/588,947A
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/588,947
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/507,968
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/122,388
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,097
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/127,598
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/130,412
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/130,696
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 60/131,278
; PRIOR FILING DATE: 1999-04-27
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; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 60/168,624
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/171,108
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/171,626
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/176,015
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/255,794
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 09/005,874
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/036,100
; PRIOR FILING DATE: 1997-01-14
; PRIOR APPLICATION NUMBER: PCT/US96/17957
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 42

RESULT 8
US-09-879-919-24
; Sequence 24, Application US/09879919
; Patent No. 6541224
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253PI
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: 60/016,812
; PRIOR FILING DATE: 1996-03-14
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-879-919-24

Query Match      92.0%; Score 1335.5; DB 4; Length 266;
Best Local Similarity 93.3%; Pred. No. 1.6e-146;
Matches 266; Conservative 0; Mismatches 0; Indels 19; Gaps 1;

QY 1 MDDSTEREQSLTSCLLKKEEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
Db 1 MDDSTEREQSLTSCLLKKEEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-588-947A-19

Query Match          92.0%; Score 1335.5; DB 4; Length 266;
Best Local Similarity 93.3%; Pred. No. 1.6e-146;
Matches 266; Conservative 0; Mismatches 0; Indels 19; Gaps 1;

QY 1 MDDSTERQSLTSCLKREEMKKECVSIILPRESPSVRSKDGKLLAATLLALLSSCC 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MDDSTERQSLTSCLKREEMKKECVSIILPRESPSVRSKDGKLLAATLLALLSSCC 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 LTVVSFYVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 LTVVSFYVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALAE 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALAE 161
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 181 KENKLVKETYGYFFYIGVLYTDKTYAMGHLIQKRVHVFGEDELSTVTLFRCTONMPETL 240
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 162 KENKLVKETYGYFFYIGVLYTDKTYAMGHLIQKRVHVFGEDELSTVTLFRCTONMPETL 221
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285
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Db 222 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 266
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RESULT 10
US-09-589-287B-28
; Sequence 28, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; PRIOR FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-28

Query Match          74.4%; Score 1080; DB 4; Length 219;
Best Local Similarity 96.3%; Pred. No. 5.5e-117;
Matches 211; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 67 YQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAPGEGNSS 126
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Db 1 YQVAAVQGDLSLRAELQGHAEKLPARAPAPKAGLGEAPAVTAGLKIFEPAPGEGNSS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 127 QNSNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALAEKENKIL 186
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 QSSNRKRAIQGAETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALAEKENKIL 120
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 187 VKETGYFFYIGVLYTDKTYAMGHLIQKRVHVFGEDELSTVTLFRCTONMPETLPNNSCY 246
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 VKETGYFFYIGVLYTDKTYAMGHLIQKRVHVFGEDELSTVTLFRCTONMPETLPNNSCY 180
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 247 SAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 181 SAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 219
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RESULT 11
US-09-588-947A-28
; Sequence 28, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C2
; CURRENT APPLICATION NUMBER: US/09/588,947A
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/588,947
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/507,968
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/122,388
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,097
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/127,598
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/130,412
; PRIOR FILING DATE: 1999-04-16
; PRIOR APPLICATION NUMBER: 60/130,696
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 60/131,278
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131,673
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: 60/136,784
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/142,659
; PRIOR FILING DATE: 1999-07-06
; PRIOR APPLICATION NUMBER: 60/145,824
; PRIOR FILING DATE: 1999-07-27
; PRIOR APPLICATION NUMBER: 60/167,239
; PRIOR FILING DATE: 1999-11-24
; PRIOR APPLICATION NUMBER: 60/168,624
; PRIOR FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: 60/171,108
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: 60/171,626
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/176,015
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: 09/255,794
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 09/005,874
; PRIOR FILING DATE: 1998-01-12
; PRIOR APPLICATION NUMBER: 60/036,100
; PRIOR FILING DATE: 1997-01-14
; PRIOR APPLICATION NUMBER: PCT/US96/17957
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-588-947A-28

Query Match          74.4%; Score 1080; DB 4; Length 219;
Best Local Similarity 96.3%; Pred. No. 5.5e-117;
Matches 211; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 67 YQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAPGEGNSS 126
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Db 1 YQVAAVQGDLSLRAELQGHAEKLPARAPAPKAGLGEAPAVTAGLKIFEPAPGEGNSS 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 127 QNSNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALAEKENKIL 186
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 QSSNRKRAIQGAETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALAEKENKIL 120
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187 VRETGYFFYIGQVLTDTYAMGHLIQRKVHVFGDELSLVTFRCIQNMPETLPNNCSY 246
QY
121 VRETGYFFYIGQVLTDTYAMGHLIQRKVHVFGDELSLVTFRCIQNMPETLPNNCSY 180
Db
247 SAGIAKLESGDELOLAIPRENAQISLDGDTFFFGALKLL 285
QY
181 SAGIAKLESGDELOLAIPRENAQISLDGDTFFFGALKLL 219
Db

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RESULT 12
US-09-589-287B-30
; Sequence 30, Application US/09589287B
; Patent No. 6403770
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Antibodies to Neutrokine-alpha
; FILE REFERENCE: PF343P3C1
; CURRENT APPLICATION NUMBER: US/09/589,287B
; CURRENT FILING DATE: 2000-06-08
; Prior application data removed - check PALM or file wrapper
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 30
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-287B-30

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Query Match	74.0%;	Score 1074;	DB 4;	Length 219;
Best Local Similarity	95.9%;	Pred. No. 2.7e-116;		
Matches 210;	Conservative	3;	Mismatches 6;	Indels 0;
Gaps	0;			

Qy	67	YQVAAIQGDLSLRAELQGHHAELKIPAGACAPKAGLEAPVATAGLKIPPEPAPGEGNSS	126
Db	1	YQVAAVQGDLSLRAELQGHHAELKIPARAPKAGLEAPVATAGLKIPPEPAPGEGNSS	60
Qy	127	QNSRNKRAVOGPEETVODCLOLADSETPTIQGSYTFVPWLLSKRGSAALEKENKIL	186
Db	61	QSSRNKRAIQGAEEVIODCLOLADSETPTIQGSYTFVPWLLSKRGSAALEKENKIL	120
Qy	187	VREGYFFTYGVLVTDKTYAMGHLIQKKVHVFGDELSLVTIFRCIQNNPETLPNNCY	246
Db	121	VREGYFFTYGVLVTDKTYAMGHLIQKKVHVFGDELSLVTIFRCIQNNPETLPNNCY	180
Qy	247	SAGIAKLEGBDELQAIAPRENAQISLQGDVTFFGALKIL	285
Db	181	SAGIAKLEGBDELQAIAPRENAOISLQGDVTFFGALKIL	219

RESULT 13
US-09-588-947A-30
; Sequence 30, Application US/09588947A
; Patent No. 6562579
; GENERAL INFORMATION:
; APPLICANT: Yu et al.
; TITLE OF INVENTION: Diagnostic Methods Using Antibodies to Neutrokin-alpha
; FILE REFERENCE: PF343P3C2
; CURRENT APPLICATION NUMBER: US/09/588.947A
; CURRENT FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/588,947
; PRIOR FILING DATE: 2000-06-08
; PRIOR APPLICATION NUMBER: 09/507,968
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: 60/122,388
; PRIOR FILING DATE: 1999-03-02
; PRIOR APPLICATION NUMBER: 60/124,097
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/126,599
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/127,598
; PRIOR FILING DATE: 1999-04-02
; PRIOR APPLICATION NUMBER: 60/130,412
; PRIOR FILING DATE: 1999-04-16

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> PRIOR APPLICATION NUMBER: 60/130,696
> PRIOR FILING DATE: 1999-04-23
> PRIOR APPLICATION NUMBER: 60/131,278
> PRIOR FILING DATE: 1999-04-27
> PRIOR APPLICATION NUMBER: 60/131,673
> PRIOR FILING DATE: 1999-04-29
> PRIOR APPLICATION NUMBER: 60/136,784
> PRIOR FILING DATE: 1999-05-28
> PRIOR APPLICATION NUMBER: 60/142,659
> PRIOR FILING DATE: 1999-07-06
> PRIOR APPLICATION NUMBER: 60/145,824
> PRIOR FILING DATE: 1999-07-27
> PRIOR APPLICATION NUMBER: 60/167,239
> PRIOR FILING DATE: 1999-11-24
> PRIOR APPLICATION NUMBER: 60/168,624
> PRIOR FILING DATE: 1999-12-03
> PRIOR APPLICATION NUMBER: 60/171,108
> PRIOR FILING DATE: 1999-12-16
> PRIOR APPLICATION NUMBER: 60/171,626
> PRIOR FILING DATE: 1999-12-23
> PRIOR APPLICATION NUMBER: 60/176,015
> PRIOR FILING DATE: 2000-01-14
> PRIOR APPLICATION NUMBER: 09/255,794
> PRIOR FILING DATE: 1999-02-23
> PRIOR APPLICATION NUMBER: 09/005,874
> PRIOR FILING DATE: 1998-01-12
> PRIOR APPLICATION NUMBER: 60/036,100
> PRIOR FILING DATE: 1997-01-14
> PRIOR APPLICATION NUMBER: PCT/US96/17957
> PRIOR FILING DATE: 1996-10-25
> NUMBER OF SEQ ID NOS: 42
> SOFTWARE: PatentIn Ver. 2.1
> SEQ ID NO 30
> LENGTH: 219
> TYPE: prt
> ORGANISM: Homo sapiens
> RS-09-568-947A-30

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Query Match	74.0%	Score 1074;	DB 4;	Length 219;
Best Local Similarity	95.9%;	Pred. No. 2.7e-116;		
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Db	1	YQVAAVOGDILASLRAELQSHHAELK	PARARAPKAGLGEAPAVTAGLKI	FEPPAPGEGNSS 60
QY	127	QNSRNKRAVOGPETVTQDCILQIADSETPT	IQKGSYTFVPWLLSFRKGSAL	EKENKIL 186
Db	61	QSSNRKAIQGAETVTQDCILQIADSETPT	IQKGSYTFVPWLLSFRKGSAL	EKENKIL 120
QY	187	VKETGYFFIYGQVLYTDKTYAMGHLI	QKRVKHVHVGDELSLVTLP	RCIQNNPETLPNNSCY 246
Db	121	VKETGYFFIYGQVLYTDKTYAMGHLI	QKRVKHVHVGDELSLVTLP	RCIQNNPETLPNNSCY 180
QY	247	SAGIAKLEEGDELQALAI	PRENAQISLDGVDVTF	FGALKLL 285
Db	181	SAGIAKLEEGDELQALAI	PRENAQISLDGVDVTF	FGALKIL 219

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RESULT 14
US-09-496-118B-5
; Sequence 5, Application US/09496118B
; Patent No. 6475986
; GENERAL INFORMATION:
; APPLICANT: Aggarwal, Bharat B.
; TITLE OF INVENTION: Uses of THANK, a TNF homologue that Activates
; TITLE OF INVENTION: Apoptosis
; FILE REFERENCE: D6206
; CURRENT APPLICATION NUMBER: US/09/496,118B
; CURRENT FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: US 60/118,531
; PRIOR FILING DATE: 1999-02-02
; NUMBER OF SEQ ID NOS: 13

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; SEQ ID NO 5
; LENGTH: 174

; TYPE: PRT
; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: domain

; LOCATION: 112..285

; OTHER INFORMATION: sequence of THANK extracellular domain

US-09-496-118B-5

Query Match 62.1%; Score 901; DB 4; Length 174;

Best Local Similarity 100.0%; Pred. No. 2.3e-96;

Matches 174; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 LKIFEPAPGEGNSQNSNRKRAVQGPETVTDCLQLIADSETPTIQSGSYTFVPWLLS 60

Qy 172 FKRGSALEEKENKILVKETGYFFIYGVLTKDYAMGHILQKRVHVFGEDELSTVTLFR 231

Db 61 FKRGSALEEKENKILVKETGYFFIYGVLTKDYAMGHILQKRVHVFGEDELSTVTLFR 120

Qy 232 CIONMPETLPNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDTFFFGALKLL 285

Db 121 CIONMPETLPNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDTFFFGALKLL 174

RESULT 15

US-09-589-287B-38

; Sequence 38, Application US/09589287B

; Patent No. 6403770

; GENERAL INFORMATION:

; APPLICANT: Yu et al.

; TITLE OF INVENTION: Antibodies to Neutrokin-alpha

; FILE REFERENCE: PF343P3C1

; CURRENT APPLICATION NUMBER: US/09/589,287B

; CURRENT FILING DATE: 2000-06-08

; Prior application data removed - check PALM or file wrapper

; NUMBER OF SEQ ID NOS: 42

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 38

; LENGTH: 289

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-589-287B-38

Query Match 54.7%; Score 793; DB 4; Length 289;

Best Local Similarity 55.0%; Pred. No. 1.8e-83;

Matches 175; Conservative 30; Mismatches 51; Indels 62; Gaps 6;

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Db 1 MDESAKTLPPPCIFCSEKGEDMKV-GYDPIFPQKEGAWFGICRGRLLAATLLALLS 59

Qy 59 CCLTVVSYFQVAALQGLASLRAELQGHAEKLPAGAGAPKAGLEEAPAVTAGLKTFEPP 118

Db 60 SSFTAMSLYQLAALQADLMNRLMELQSYRGSAATPAAAGAPE-----LTAGVKLLTPA 111

Qy 119 APCEGNSQNSNRKRAVQGPET-----VTQDCL 147

Db 112 APRPHNSRGRNRRAFGQPEETEQQVDLSAPPAPCLPCGRHSQHDNDGMNLRNTIQDCL 171

Qy 148 QLIIADSETPTIQSGSYTFVPWLLSFKRGSALEEKENKILVKETGYFFIYGVLTKDYA 207

Db 172 QLIIADSDTP-----ALBEKENKIVRQTGYFFIYSQVLYTDPIFA 211

Qy 208 MGHILQKRVHVFGEDELSTVTLFRCLQNNMPETLPNNSCYSAGIAKLEEGDELQLAIPREN 267

Db 212 MGHVIOKRVHVFGEDELSTVTLFRCLQNNMPKTLNNSCYSAGIARLEEGDELQLAIPREN 271

Qy 268 AQISLDGDTFFFGALKLL 285

Db 272 AQISRGDDTFFFGALKLL 289

Search completed: August 28, 2003, 18:06:51
Job time : 19 secs

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OM protein - protein search, using sw model

Run on: August 28, 2003, 18:05:47 ; Search time 60 seconds
(without alignments)
649.714 Million cell updates/sec

Title: US-09-507-968D-2
Perfect score: 1451
Sequence: 1 MDSTEREQSLKRE.....ENAIQSLDGVTFGALKLL 285

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 510680 seqs, 136781880 residues
Total number of hits satisfying chosen parameters: 510680

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1451	100.0	285	9 US-09-193-663-2	Sequence 2, Appli
3	1451	100.0	285	9 US-09-877-156-1	Sequence 1, Appli
4	1451	100.0	285	9 US-09-879-919-23	Sequence 23, Appli
5	1451	100.0	285	10 US-09-929-493-2	Sequence 2, Appli
6	1451	100.0	285	10 US-09-779-050A-2	Sequence 2, Appli
7	1451	100.0	285	11 US-09-302-863-4	Sequence 4, Appli
8	1451	100.0	285	11 US-09-880-748-3228	Sequence 3228, Ap
9	1451	100.0	285	11 US-09-932-613-173	Sequence 173, Ap
10	1451	100.0	285	12 US-10-137-870-24	Sequence 24, Appli
11	1451	100.0	285	12 US-10-140-018-24	Sequence 24, Appli
12	1451	100.0	285	12 US-10-140-021-24	Sequence 24, Appli
13	1451	100.0	285	12 US-10-140-274-24	Sequence 24, Appli
14	1451	100.0	285	12 US-10-140-471-24	Sequence 24, Appli
15	1451	100.0	285	12 US-10-140-807-24	Sequence 24, Appli

16	1451	100.0	285	12 US-10-140-922-24	Sequence 24, Appli
17	1451	100.0	285	12 US-10-140-924-24	Sequence 24, Appli
18	1451	100.0	285	12 US-10-140-926-24	Sequence 24, Appli
19	1451	100.0	285	12 US-10-141-698-24	Sequence 24, Appli
20	1451	100.0	285	12 US-10-141-702-24	Sequence 24, Appli
21	1451	100.0	285	12 US-10-141-704-24	Sequence 24, Appli
22	1451	100.0	285	12 US-10-142-421-24	Sequence 24, Appli
23	1451	100.0	285	12 US-10-142-432-24	Sequence 24, Appli
24	1451	100.0	285	12 US-10-142-767-24	Sequence 24, Appli
25	1451	100.0	285	12 US-10-143-033-24	Sequence 24, Appli
26	1451	100.0	285	12 US-10-144-994-24	Sequence 24, Appli
27	1451	100.0	285	12 US-10-145-628-24	Sequence 24, Appli
28	1451	100.0	285	12 US-10-145-631-24	Sequence 24, Appli
29	1451	100.0	285	12 US-10-145-633-24	Sequence 24, Appli
30	1451	100.0	285	12 US-10-145-746-24	Sequence 24, Appli
31	1451	100.0	285	12 US-10-145-748-24	Sequence 24, Appli
32	1451	100.0	285	12 US-10-145-823-24	Sequence 24, Appli
33	1451	100.0	285	12 US-10-145-826-24	Sequence 24, Appli
34	1451	100.0	285	12 US-10-145-870-24	Sequence 24, Appli
35	1451	100.0	285	12 US-10-145-876-24	Sequence 24, Appli
36	1451	100.0	285	12 US-10-145-959-24	Sequence 24, Appli
37	1451	100.0	285	12 US-10-146-724-24	Sequence 24, Appli
38	1451	100.0	285	12 US-10-146-725-24	Sequence 24, Appli
39	1451	100.0	285	12 US-10-146-795-24	Sequence 24, Appli
40	1451	100.0	285	12 US-10-147-495-24	Sequence 24, Appli
41	1451	100.0	285	12 US-10-147-501-24	Sequence 24, Appli
42	1451	100.0	285	12 US-10-147-504-24	Sequence 24, Appli
43	1451	100.0	285	12 US-10-147-506-24	Sequence 24, Appli
44	1451	100.0	285	12 US-10-147-509-24	Sequence 24, Appli
45	1451	100.0	285	12 US-10-147-510-24	Sequence 24, Appli

ALIGNMENTS

RESULT 1
US-08-971-317A-2
; Sequence 2, Application US/08971317A
; Publication No. US20010010925A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES
; TITLE OF INVENTION: THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,317A
; FILING DATE: 17-NOV-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Goller, Mimi C
; REGISTRATION NUMBER: 39,046
; REFERENCE/DOCKET NUMBER: 6255.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (847) 935-7550
; TELEFAX: (847) 938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:

293308123370

; LENGTH: 285 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. US20010010925A1e
US-08-971-317A-2

Query Match
Best Local Similarity 100.0%; Score 1451; DB 8; Length 285;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTEREQSLTSLCKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
Db 1 MDSTEREQSLTSLCKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
QY 61 LTWVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
Db 61 LTWVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
QY 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
Db 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQKRVHVFGEDELSTLFRCIQNMPTL 240
Db 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQKRVHVFGEDELSTLFRCIQNMPTL 240
QY 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDTFFGALKLL 285
Db 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDTFFGALKLL 285

RESULT 2

US-09-193-663-2
; Sequence 2, Application US/09193663
; Patent No. US20020055624A1
; GENERAL INFORMATION:
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: TNF-DELTA LIGAND AND USES THEREOF
; FILE REFERENCE: 6255.US.02
; CURRENT APPLICATION NUMBER: US/09/193,663
; EARLIER FILING DATE: 1998-11-17
; EARLIER APPLICATION NUMBER: 60/065,916
; EARLIER FILING DATE: 1997-11-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-663-2

Query Match
Best Local Similarity 100.0%; Score 1451; DB 9; Length 285;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTEREQSLTSLCKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
Db 1 MDSTEREQSLTSLCKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
QY 61 LTWVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
Db 61 LTWVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
QY 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
Db 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQKRVHVFGEDELSTLFRCIQNMPTL 240
Db 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQKRVHVFGEDELSTLFRCIQNMPTL 240
QY 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDTFFGALKLL 285

10/165,738

Db 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDTFFGALKLL 285

RESULT 3
US-09-877-156-1
; Sequence 1, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
; APPLICANT: Catharine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNF FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/877,156
; CURRENT FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/286,529
; PRIOR FILING DATE: 1998-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 285
; TYPE: PRT
; ORGANISM: human
US-09-877-156-1

Query Match
Best Local Similarity 100.0%; Score 1451; DB 9; Length 285;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDSTEREQSLTSLCKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
Db 1 MDSTEREQSLTSLCKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
QY 61 LTWVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
Db 61 LTWVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
QY 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
Db 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSALEE 180
QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQKRVHVFGEDELSTLFRCIQNMPTL 240
Db 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQKRVHVFGEDELSTLFRCIQNMPTL 240
QY 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDTFFGALKLL 285
Db 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDTFFGALKLL 285

RESULT 4

US-09-879-919-23
; Sequence 23, Application US/09879919
; Patent No. US20020064829A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang, et al.
; TITLE OF INVENTION: Human Tumor Necrosis Factor Delta and Epsilon
; FILE REFERENCE: PF253P1
; CURRENT APPLICATION NUMBER: US/09/879,919
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,978
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/254,875
; PRIOR FILING DATE: 2000-12-13
; PRIOR APPLICATION NUMBER: 60/241,952
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/211,537
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 08/815,783
; PRIOR FILING DATE: 1997-03-12

; PRIOR APPLICATION NUMBER: 60/016,812
 ; PRIOR FILING DATE: 1996-03-14
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 23
 ; LENGTH: 285
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-879-919-23

Query Match 100.0%; Score 1451; DB 9; Length 285;
 Best Local Similarity 100.0%; Pred. No. 2.9e-139;
 Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDDSTEREQSLTSCLEKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
 Db 1 MDDSTEREQSLTSCLEKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
 QY 61 LTVVSFYQVAALQGDLSLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
 Db 61 LTVVSFYQVAALQGDLSLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
 QY 121 GEGNSSONSRRKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVFWLLSFKRGSAL 180
 Db 121 GEGNSSONSRRKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVFWLLSFKRGSAL 180
 QY 181 KENKILVKETGYFFIYGVLYTDKTYAMGHLIQRKKVHVFGDELSLTVLFRCIQNMPTL 240
 Db 181 KENKILVKETGYFFIYGVLYTDKTYAMGHLIQRKKVHVFGDELSLTVLFRCIQNMPTL 240
 QY 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVTFFGALKLL 285
 Db 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVTFFGALKLL 285

RESULT 5
 US-09-929-493-2
 ; Sequence 2, Application US/09929493
 ; Patent No. US2002011512A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yu et al.
 ; TITLE OF INVENTION: Neutrokin-alpha and Neutrokin-alpha Splice Variant
 ; FILE REFERENCE: PF343P4
 ; CURRENT APPLICATION NUMBER: US/09/929,493
 ; PRIOR FILING DATE: 2001-08-15
 ; PRIOR APPLICATION NUMBER: 60/225,628
 ; PRIOR FILING DATE: 2000-08-15
 ; PRIOR APPLICATION NUMBER: 60/227,008
 ; PRIOR FILING DATE: 2000-08-23
 ; PRIOR APPLICATION NUMBER: 60/234,338
 ; PRIOR FILING DATE: 2000-09-22
 ; PRIOR APPLICATION NUMBER: 60/240,806
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/250,020
 ; PRIOR FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-06
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/296,122
 ; PRIOR FILING DATE: 2001-06-07
 ; PRIOR APPLICATION NUMBER: 60/304,809
 ; PRIOR FILING DATE: 2001-07-13
 ; NUMBER OF SEQ ID NOS: 47
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 285
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-929-493-2

Query Match 100.0%; Score 1451; DB 10; Length 285;
 Best Local Similarity 100.0%; Pred. No. 2.9e-139;

Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDDSTEREQSLTSCLEKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
 Db 1 MDDSTEREQSLTSCLEKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
 QY 61 LTVVSFYQVAALQGDLSLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
 Db 61 LTVVSFYQVAALQGDLSLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
 QY 121 GEGNSSONSRRKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVFWLLSFKRGSAL 180
 Db 121 GEGNSSONSRRKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVFWLLSFKRGSAL 180
 QY 181 KENKILVKETGYFFIYGVLYTDKTYAMGHLIQRKKVHVFGDELSLTVLFRCIQNMPTL 240
 Db 181 KENKILVKETGYFFIYGVLYTDKTYAMGHLIQRKKVHVFGDELSLTVLFRCIQNMPTL 240
 QY 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVTFFGALKLL 285
 Db 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVTFFGALKLL 285

RESULT 6
 US-09-779-050A-2
 ; Sequence 2, Application US/09779050A
 ; Patent No. US20020160416A1
 ; GENERAL INFORMATION:
 ; APPLICANT: BOYLE, WILLIAM
 ; APPLICANT: HSU, HAILING
 ; TITLE OF INVENTION: RECEPTOR FROM TNF FAMILY
 ; FILE REFERENCE: A-570B
 ; CURRENT APPLICATION NUMBER: US/09/779,050A
 ; CURRENT FILING DATE: 2001-02-12
 ; PRIOR APPLICATION NUMBER: 60/181,800
 ; PRIOR FILING DATE: 2000-02-11
 ; NUMBER OF SEQ ID NOS: 52
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 285
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-779-050A-2

Query Match 100.0%; Score 1451; DB 10; Length 285;
 Best Local Similarity 100.0%; Pred. No. 2.9e-139;
 Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDDSTEREQSLTSCLEKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
 Db 1 MDDSTEREQSLTSCLEKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
 QY 61 LTVVSFYQVAALQGDLSLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
 Db 61 LTVVSFYQVAALQGDLSLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
 QY 121 GEGNSSONSRRKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVFWLLSFKRGSAL 180
 Db 121 GEGNSSONSRRKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVFWLLSFKRGSAL 180
 QY 181 KENKILVKETGYFFIYGVLYTDKTYAMGHLIQRKKVHVFGDELSLTVLFRCIQNMPTL 240
 Db 181 KENKILVKETGYFFIYGVLYTDKTYAMGHLIQRKKVHVFGDELSLTVLFRCIQNMPTL 240
 QY 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVTFFGALKLL 285
 Db 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVTFFGALKLL 285

RESULT 7
 US-09-302-863-4
 ; Sequence 4, Application US/09302863
 ; Publication No. US2003002223A1

```

; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G
; TITLE OF INVENTION: METHODS OF USE OF THE TAC1/TAC1-L INTERACTION
; FILE REFERENCE: 2519
; CURRENT APPLICATION NUMBER: US/09/302,863
; CURRENT FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 4
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Human
US-09-302-863-4

Query Match      100.0%; Score 1451; DB 11; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.9e-139;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
QY 61 LTVVSFYQVAALQGDLSLRAELQGHHAELKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
DB 61 LTVVSFYQVAALQGDLSLRAELQGHHAELKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
QY 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALAE 180
DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALAE 180
QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLCFRCIONMPETL 240
DB 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLCFRCIONMPETL 240
QY 241 PNNCSYSAGIAKLEEGDELQLAIPRENAQISLDGDTVFFGALKLL 285
DB 241 PNNCSYSAGIAKLEEGDELQLAIPRENAQISLDGDTVFFGALKLL 285

RESULT 8
US-09-880-748-3228
; Sequence 3228, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Bly5
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 3228
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-3228

Query Match      100.0%; Score 1451; DB 11; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.9e-139;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
QY 61 LTVVSFYQVAALQGDLSLRAELQGHHAELKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
DB 61 LTVVSFYQVAALQGDLSLRAELQGHHAELKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
QY 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALAE 180
DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALAE 180
QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLCFRCIONMPETL 240
DB 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLCFRCIONMPETL 240
QY 241 PNNCSYSAGIAKLEEGDELQLAIPRENAQISLDGDTVFFGALKLL 285
DB 241 PNNCSYSAGIAKLEEGDELQLAIPRENAQISLDGDTVFFGALKLL 285

RESULT 9
US-09-932-613-173
; Sequence 173, Application US/09932613
; Publication No. US20030091565A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; APPLICANT: Beltzer, James P.
; APPLICANT: Potter, M. Daniel
; APPLICANT: Fleming, Tony J.
; APPLICANT: Rosen, Craig A.
; TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
; FILE REFERENCE: Dyx-025.1 PCT; DYX-025.1 US
; CURRENT APPLICATION NUMBER: US/09/932,613
; CURRENT FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 173
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-932-613-173

Query Match      100.0%; Score 1451; DB 11; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.9e-139;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
QY 61 LTVVSFYQVAALQGDLSLRAELQGHHAELKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
DB 61 LTVVSFYQVAALQGDLSLRAELQGHHAELKLPAGAGAPKAGLEAPAVTAGLKIFEPPAP 120
QY 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALAE 180
DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALAE 180
QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLCFRCIONMPETL 240
DB 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTLCFRCIONMPETL 240
QY 241 PNNCSYSAGIAKLEEGDELQLAIPRENAQISLDGDTVFFGALKLL 285
DB 241 PNNCSYSAGIAKLEEGDELQLAIPRENAQISLDGDTVFFGALKLL 285

RESULT 10
US-10-137-870-24
; Sequence 24, Application US/10137870
; Publication No. US20030138883A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
```

APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C155
CURRENT APPLICATION NUMBER: US/10/137,870
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 24
LENGTH: 285
TYPE: PRT
ORGANISM: Homo Sapien
US-10-137-870-24

Query Match 100.0%; Score 1451; DB 12; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.9e-139;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDDSTEREQSLTSCLLKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
DB 1 MDDSTEREQSLTSCLLKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
QY 61 LTVVSFYQVAALQGDLSLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
DB 61 LTVVSFYQVAALQGDLSLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
QY 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQGSLYTFVPWLLSFKRGSAL 180
DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQGSLYTFVPWLLSFKRGSAL 180
QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQKRVHVFGEDELSTLFRCIQNMPE 240
DB 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQKRVHVFGEDELSTLFRCIQNMPE 240
QY 241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGVTFFFGALKLL 285
DB 241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGVTFFFGALKLL 285

RESULT 11
US-10-140-018-24
Sequence 24, Application US/10140018
Publication No. US20030138886A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.

APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C158
CURRENT APPLICATION NUMBER: US/10/140,018
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 24
LENGTH: 285
TYPE: PRT
ORGANISM: Homo Sapien
US-10-140-018-24

Query Match 100.0%; Score 1451; DB 12; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.9e-139;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDDSTEREQSLTSCLLKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
DB 1 MDDSTEREQSLTSCLLKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
QY 61 LTVVSFYQVAALQGDLSLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
DB 61 LTVVSFYQVAALQGDLSLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
QY 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQGSLYTFVPWLLSFKRGSAL 180
DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQGSLYTFVPWLLSFKRGSAL 180
QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQKRVHVFGEDELSTLFRCIQNMPE 240
DB 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQKRVHVFGEDELSTLFRCIQNMPE 240
QY 241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGVTFFFGALKLL 285
DB 241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGVTFFFGALKLL 285

RESULT 12
US-10-140-021-24
Sequence 24, Application US/10140021
Publication No. US20030138886A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3330R1C167
CURRENT APPLICATION NUMBER: US/10/140,021
CURRENT FILING DATE: 2002-05-06
Prior Application removed - See Palm or File Wrapper
NUMBER OF SEQ ID NOS: 550
SEQ ID NO 24
LENGTH: 285
TYPE: PRT

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; ORGANISM: Homo Sapien
US-10-140-021-24

Query Match      100.0%; Score 1451; DB 12; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.9e-139;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDDSTEREQSLTSCILKREEMKKECVSILPKRESVSRSSKDGKLLAATLLALLSCC 60
DB 1 MDDSTEREQSLTSCILKREEMKKECVSILPKRESVSRSSKDGKLLAATLLALLSCC 60

QY 61 LTVVSFYQVAALQDGLASLRAELQGHHAELKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
DB 61 LTVVSFYQVAALQDGLASLRAELQGHHAELKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120

QY 121 GEGNSSONSNRKRAVQGPETVTQDCQLQIADSETPTIQKGSYTFVFWLLSFKRGSAL EE 180
DB 121 GEGNSSONSNRKRAVQGPETVTQDCQLQIADSETPTIQKGSYTFVFWLLSFKRGSAL EE 180

QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFLFRCIQNM PETL 240
DB 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFLFRCIQNM PETL 240

QY 241 PNNCSYAGIAKLEEGDELOLAIPRENAQISLDGVDVTFFGALKLL 285
DB 241 PNNCSYAGIAKLEEGDELOLAIPRENAQISLDGVDVTFFGALKLL 285

RESULT 13
US-10-140-274-24
; Sequence 24, Application US/10140274
; Publication No. US20030143674A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC161
; CURRENT APPLICATION NUMBER: US/10/140,274
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 24
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-274-24

Query Match      100.0%; Score 1451; DB 12; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.9e-139;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDDSTEREQSLTSCILKREEMKKECVSILPKRESVSRSSKDGKLLAATLLALLSCC 60
DB 1 MDDSTEREQSLTSCILKREEMKKECVSILPKRESVSRSSKDGKLLAATLLALLSCC 60

QY 61 LTVVSFYQVAALQDGLASLRAELQGHHAELKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
DB 61 LTVVSFYQVAALQDGLASLRAELQGHHAELKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120

QY 121 GEGNSSONSNRKRAVQGPETVTQDCQLQIADSETPTIQKGSYTFVFWLLSFKRGSAL EE 180
DB 121 GEGNSSONSNRKRAVQGPETVTQDCQLQIADSETPTIQKGSYTFVFWLLSFKRGSAL EE 180

QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFLFRCIQNM PETL 240
DB 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFLFRCIQNM PETL 240

QY 241 PNNCSYAGIAKLEEGDELOLAIPRENAQISLDGVDVTFFGALKLL 285
DB 241 PNNCSYAGIAKLEEGDELOLAIPRENAQISLDGVDVTFFGALKLL 285

RESULT 14
US-10-140-471-24
; Sequence 24, Application US/10140471
; Publication No. US20030138887A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330RIC163
; CURRENT APPLICATION NUMBER: US/10/140,471
; CURRENT FILING DATE: 2002-05-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 24
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-471-24

Query Match      100.0%; Score 1451; DB 12; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.9e-139;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDDSTEREQSLTSCILKREEMKKECVSILPKRESVSRSSKDGKLLAATLLALLSCC 60
DB 1 MDDSTEREQSLTSCILKREEMKKECVSILPKRESVSRSSKDGKLLAATLLALLSCC 60

QY 61 LTVVSFYQVAALQDGLASLRAELQGHHAELKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
DB 61 LTVVSFYQVAALQDGLASLRAELQGHHAELKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120

QY 121 GEGNSSONSNRKRAVQGPETVTQDCQLQIADSETPTIQKGSYTFVFWLLSFKRGSAL EE 180
DB 121 GEGNSSONSNRKRAVQGPETVTQDCQLQIADSETPTIQKGSYTFVFWLLSFKRGSAL EE 180

QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFLFRCIQNM PETL 240
DB 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKKVHVFGDELSLVTFLFRCIQNM PETL 240

QY 241 PNNCSYAGIAKLEEGDELOLAIPRENAQISLDGVDVTFFGALKLL 285
DB 241 PNNCSYAGIAKLEEGDELOLAIPRENAQISLDGVDVTFFGALKLL 285
```

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RESULT 15
US-10-140-807-24
; Sequence 24, Application US/10140807
; Publication No. US20030134354A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: Deforge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3330P1C174
; CURRENT APPLICATION NUMBER: US/10/140,807
; CURRENT FILING DATE: 2002-05-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO 24
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-140-807-24

Query Match      100.0%; Score 1451; DB 12; Length 285;
Best Local Similarity 100.0%; Pred. No. 2.9e-139;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDDSTEREQSRLTSLCKKREMKKECVSILPRKESPSVRSSKDGKLLAATLLIALISCC 60
Db 1 MDDSTEREQSRLTSLCKKREMKKECVSILPRKESPSVRSSKDGKLLAATLLIALISCC 60

QY 61 LTVVSFYQVAALQDGLASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
Db 61 LTVVSFYQVAALQDGLASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120

QY 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQGSYTFVPWLLSEKRGSALEE 180
Db 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQGSYTFVPWLLSEKRGSALEE 180

QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQKKVHVFGDELSLVTLFRCIQNMPEL 240
Db 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQKKVHVFGDELSLVTLFRCIQNMPEL 240

QY 241 PNNSCYSAGIAKLEEGDELQIAIPRENAQISLDGDDVTFFGALKLL 285
Db 241 PNNSCYSAGIAKLEEGDELQIAIPRENAQISLDGDDVTFFGALKLL 285

Search completed: August 28, 2003, 18:14:54
Job time : 61 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 17:59:46 ; Search time 23 seconds
(without alignments)
582.722 Million cell updates/sec

Title: US-09-507-968d-2

Perfect score: 1451

Sequence: 1 MDDSTEREQSLTSLCKRE.....ENAIQISLDGVDVTFGALKLL 285

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1451	100.0	285	1	T13B_HUMAN
2	910	62.7	309	1	T13B_MOUSE
3	246.5	17.0	241	1	TN13_MOUSE
4	244.5	16.9	250	1	TN13_HUMAN
5	118.5	8.2	233	1	TNFA_CANFA
6	116.5	8.0	233	1	TNFA_TURTR
7	111.5	7.7	233	1	TNFA_FELCA
8	110.5	7.6	233	1	TNFA_DELLE
9	110.5	7.6	235	1	TNFA_RAT
10	109.5	7.5	235	1	TNFA_MOUSE
11	108	7.4	233	1	TNFA_BOVIN
12	107.5	7.4	235	1	TNFA_PERLE
13	107	7.4	232	1	TNFA_PIG
14	106.5	7.3	234	1	TNFA_CAPHI
15	105.5	7.3	233	1	TNFA_LANGL
16	104	7.2	232	1	TNFA_PANTR
17	103.5	7.1	234	1	TNFA_BOSIN
18	103	7.1	233	1	TNFA_BUBBU
19	103	7.1	391	1	EDA_BOVIN
20	102.5	7.1	391	1	TNFA_SHEEP
21	102.5	7.1	391	1	EDA_HUMAN
22	102.5	7.1	391	1	EDA_MOUSE
23	101.5	7.0	229	1	TNFA_CEREL
24	100.5	6.9	205	1	TNFB_HUMAN
25	99	6.8	234	1	TNFA_CAVPO
26	98.5	6.8	233	1	TNFA_HUMAN
27	97.5	6.7	184	1	YGF_PSEAE
28	97.5	6.7	281	1	TNFB_HUMAN
29	97	6.7	281	1	TN10_HUMAN
30	95.5	6.6	233	1	TNFA_SALSC
31	95.5	6.6	280	1	TNFB_MACMU
32	95	6.5	233	1	TNFA_TRIVU
33	93.5	6.4	235	1	TNFA_RABIT

34	93.5	6.4	282	1	TNFB_PIG
35	93.5	6.4	651	1	E2BD_YEAST
36	92.5	6.4	253	1	TNFA_SPAAU
37	92.5	6.4	280	1	TNFB_CERTO
38	90.5	6.2	204	1	TNFB_PIG
39	89.5	6.2	233	1	TNFA_PAPSP
40	89.5	6.2	234	1	TNFA_HORSE
41	89	6.1	1267	1	HMT1_HUMAN
42	87.5	6.0	233	1	TNFA_PAPAN
43	87.5	6.0	233	1	TNFA_PAPHU
44	87.5	6.0	993	1	TSH_DROME
45	86.5	6.0	233	1	TNFA_MARMO

ALIGNMENTS

RESULT 1	
T13B_HUMAN	
ID T13B_HUMAN	STANDARD; PRT; 285 AA.
AC Q9Y275;	
DT 16-OCT-2001 (Rel. 40, Created)	
DT 16-OCT-2001 (Rel. 40, Last sequence update)	
DT 15-SEP-2003 (Rel. 42, Last annotation update)	
DE Tumor necrosis factor ligand superfamily member 13B (TNF-and APOL-	
DE related leukocyte expressed ligand 1) (TALL-1) (B lymphocyte	
DE stimulator) (Blys) (B cell-activating factor) (BAFF) (dendritic cell-	
DE derived TNF-like molecule).	
GN TNFSF13B OR TALL1 OR BLYS OR BAFF OR ZTNF4.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RX MEDLINE=99260341; PubMed=10331498;	
RA Shu H.-B., Hu W.-H., Johnson H.;	
RT "TALL-1 is a novel member of the TNF family that is down-regulated by	
RT mitogens.";	
RL J. Leukoc. Biol. 65:680-683(1999).	
RN [2]	
RP SEQUENCE FROM N.A., AND SEQUENCE OF 134-148.	
RX MEDLINE=99288033; PubMed=10359578;	
RA Schneider P., MacKay F., Steiner V., Hofmann K., Bodmer J.-L.,	
RA Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H.,	
RA Valmori D., Romero P., Werner-Favre C., Zubler R.H., Browning J.L.,	
RA Tschoopp J.;	
RT "BAFF, a novel ligand of the tumor necrosis factor family, stimulates	
RT B cell growth.";	
-RL J. Exp. Med. 189:1747-1756(1999).	
RN [3]	
RP SEQUENCE FROM N.A.	
RC TISSUE=Monocytes, and Neutrophils;	
RX MEDLINE=99329343; PubMed=10398604;	
RA Moore P.A., Belvedere O., Orr A., Pieri K., Lafleur D.W., Feng P.,	
RA Soppet D.A., Charters M., Gentz R., Parmelee D., Li Y., Galperina O.,	
RA Giri J., Roschke V., Nardelli B., Carrelli J., Sosnovtseva S.,	
RA Greenfield W., Ruben S.M., Olsen H.S., Fikes J., Hilbert D.M.;	
RT "Blys: member of the tumor necrosis factor family and B lymphocyte	
RT stimulator.";	
RL Science 285:260-263(1999).	
RN [4]	
RP SEQUENCE FROM N.A.	
RA Farrah T., Gross J., Piddington C., O'Hara P.;	
RT "Homo sapiens homolog of tumor necrosis factor.";	
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.	
RN [5]	
RP SEQUENCE FROM N.A.	
RC TISSUE=Dendritic cell;	
RA Zhang W., Wan T., Yu Y., Cao X.;	
RT "A novel dendritic cell-derived TNF-like molecule.";	
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.	
RN [6]	

Query Match 100.0%; Score 1451; DB 1; Length 285;
 Best Local Similarity 100.0%; Pred. No. 1.9e-116;
 Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDDSTERQSLTSCLEKREMKKECVSILPKRSPSVRSKDGKLLAATLLALLSCC 60
 DB 1 MDDSTERQSLTSCLEKREMKKECVSILPKRSPSVRSKDGKLLAATLLALLSCC 60

QY 61 LTVSVFYVAAALQDGLASRAELQGHAEKLPAGAPKAGLEAPAVTAGLIFPEPPAP 120
 DB 61 LTVSVFYVAAALQDGLASRAELQGHAEKLPAGAPKAGLEAPAVTAGLIFPEPPAP 120

QY 121 GEGNSSQNSRNKRAVOGPEETVTQDCLQLIADSETPTIQKSGYTFVPWLLSFKRGSALEE 180
 DB 121 GEGNSSQNSRNKRAVOGPEETVTQDCLQLIADSETPTIQKSGYTFVPWLLSFKRGSALEE 180

QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKVVHFGDELSLVTFRCIQNNPETL 240
 DB 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQRKVVHFGDELSLVTFRCIQNNPETL 240

QY 241 PNNSCYSAGIAKLEEGDELQALIPRENAQISLDGVTFFGALKLL 285
 DB 241 PNNSCYSAGIAKLEEGDELQALIPRENAQISLDGVTFFGALKLL 285

RESULT 2
 T13B_MOUSE
 ID T13B_MOUSE STANDARD; PRT; 309 AA.
 AC Q9WU72;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 13B (B cell-activating factor) (BAFF).
 GN TNFSF13B OR BAFF.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=99288033; PubMed=10359578;
 RA Schneider P., Mackay F., Steiner V., Hofmann K., Bodmer J.-L.,
 RA Holler N., Ambrose C., Lawton P., Bixler S., Acha-Orbea H.,
 RA Valmorri D., Romero P., Werner-Favre C., Zubler R.H., Browning J.L.,
 RA Tschopp J.;
 RT "BAFF, a novel ligand of the tumor necrosis factor family, stimulates B cell growth.";
 RL J. Exp. Med. 189:1747-1756(1999).
 [2]
 SEQUENCE FROM N.A., AND VARIANT SER-79.
 RC STRAIN=NZB;
 RX MEDLINE=21850530; PubMed=11862414;
 RA Jiang Y., Ohtsui M., Abe M., Li N., Xiu Y., Wen X.S., Shirai T.,
 RA Hirose S.;
 RT "Polymorphism and chromosomal mapping of the mouse gene for B-cell activating factor belonging to the tumor necrosis factor family (Baff) and association with the autoimmune phenotype.";
 RL Immunogenetics 53:810-813(2001).
 CC -1- FUNCTION: Cytokine that binds to TNFSF13B/TACI and TNFSF17/BCMA. TNFSF13/APRIL binds to the same 2 receptors. Together, they form a 2 ligands -2 receptors pathway involved in the stimulation of B- and T-cell function and the regulation of humoral immunity. A third B-cell specific BAFF-receptor (BAFFR/BR3) promotes the survival of mature B-cells and the B-cell response.
 CC -1- SUBUNIT: Homotrimer.
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.
 CC -1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING.
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.

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 CC -----
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 CC MGI; 1344376; Tnfsf13b.
 CC InterPro; IPR006052; TnF_family.
 CC SMART; SM00207; TNF; 1.
 CC PROSITE; PS00251; TNF_1; FALSE_NEG.
 CC PROSITE; PS50049; TNF_2; 1.
 CC Cytokine; Transmembrane; Glycoprotein; Signal-anchor;
 KW Polymorphism.
 FT CHAIN 1 309 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT MEMBER 13B, MEMBRANE FORM.
 FT CHAIN 127 309 TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY
 FT MEMBER 13B, SOLUBLE FORM.
 FT DOMAIN 1 47 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 48 68 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 69 309 EXTRACELLULAR (POTENTIAL).
 FT SITE 126 127 CLEAVAGE (BY SIMILARITY).
 FT DISULFID 256 269 BY SIMILARITY.
 FT CARBOHYD 117 117 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 266 266 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARIANT 79 79 N -> S (IN STRAIN NZB).
 SQ SEQUENCE 309 AA; 34192 MW; F3DE6056B6034B4 CRC64;

Query Match 62.7%; Score 910; DB 1; Length 309;
 Best Local Similarity 60.4%; Pred. No. 2.8e-70;
 Matches 192; Conservative 33; Mismatches 51; Indels 42; Gaps 5;

QY 1 MDDSTER-EQSLTSCLEKREMKKECVSILPKRSPS-VRSKDGKLLAATLLALLS 58
 DB 1 MDESATLPPPCLCFCSEKGEDMKV-GYDPTPQKEGAWFGICRDGRLAATLLALLS 59

QY 59 CCLTVSVFYVAAALQDGLASRAELQGHAEKLPAGAPKAGLEAPAVTAGLIFPEPP 118
 DB 60 SSFTAMSLYQLAAQALQALMLNRLMELQSYRGSATFAAGAPE-----LTAGVKLLTPA 111

QY 119 APGESSQNSRNKRAVOGPEET-----VTQDCL 147
 DB 112 APRHNSRGHRNRRAFGQPEETEDVDLSAPPAPCLPGCRHSQDDHGMNRLNIQDCL 171

QY 148 QLIADSETPTIQKSGYTFVPWLLSFKRGSALEEKENKILVKETGYFFIYGQVLYTDKTYA 207
 DB 172 QLIADSDPTIRKGYTFVPWLLSFKRGNALEEKENKIVVRQTYGFFIYSQVLYTDPIFA 231

QY 208 MGHILQRKVVHFGDELSLVTFRCIQNNPETLNNSCYSAGIAKLEEGDELQALIPREN 267
 DB 232 MGHVLRKRVHFGDELSLVTFRCIQNNPKTLNNSCYSAGIARLEEGDEQLAIPREN 291

QY 268 AQISLDGVTFFGALKLL 285
 DB 292 AQISRNGDVTFFGALKLL 309

RESULT 3
 TN13_MOUSE
 ID TN13_MOUSE STANDARD; PRT; 241 AA.
 AC Q9D777; Q9ERP1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 13 (A proliferation-inducing ligand) (APRIL).
 DE TNFSF13 OR APRIL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=21170294; PubMed=10973284;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stollina M.,
 RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
 RT "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
 humoral immunity";
 RL Nat. Immunol. 1:252-256(2000).
 [2]
 SEQUENCE FROM N.A.
 RP MEDLINE=C57BL/6J; TISSUE=Tongue;
 RX STRAIN=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -!- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and to
 CC TNFRSF17/BCMA. May be implicated in the regulation of tumor cell
 CC growth. May be involved in monocyte/macrophage-mediated
 CC immunological processes.
 CC -!- SUBUNIT: Homotrimer (Potential).
 CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
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 CC -----
 DR EMBL: AF294825; AAG22534.1; -;
 DR EMBL: AK009514; BAB26332.1; -;
 DR MGD: MGI:1916833; Tnfrsf13.
 DR GO: GO:0008284; P:positive regulation of cell proliferation; IDA.
 DR InterPro: IPR006052; TNF_family.
 DR Pfam: PF00229; TNF; 1.
 DR SMART: SM00207; TNF; 1.
 DR PROSITE: PS00251; TNF_1; 1.
 DR PROSITE: PS50049; TNF_2; 1.
 DR CYTOKINE: Immune response; Glycoprotein.
 KW CYTOKINE; Immune response; Glycoprotein.
 FT PROPEP 1 95
 FT CHAIN 96 241
 FT SITE 95 96
 FT DISULFID 187 202
 FT CARBOHYD 115 115
 FT N-LINKED (GLCNAC...) (POTENTIAL).
 FT CONFLICT 120 120
 FT MISSING (IN REF. 2).
 SQ SEQUENCE 241 AA; 26889 MW; 4896D03BDBC712A4 CRC64;
 Query Match 17.0%; Score 246.5; DB 1; Length 241;
 Best Local Similarity 30.1%; Pred. No. 7.7e-14;
 Matches 75; Conservative 40; Mismatches 81; Indels 53; Gaps 9;
 QY 53 LLALLSCCLTVVSVFYQVAALQGLASLRAELQGHAEKLPAGAGAPKAG-----LSEA 105
 Db 29 VLGVATCAVALL-----LQQLSLRREV-----SRQSRGPGSKQGRWQSLWEQS 78
 QY 106 PAVTAGLKIFEPAPAGEGNSNSNRKRAVOGPEETVTQDCIQLI-----ADSETPTI 158
 Db 79 PDVLEAWK-----DGAKRRRAVLTKQKKKHSVHLVVPVNTSKADSDV--- 124
 QY 159 QKGSYTFVFWLLSFKRGSALEKENKILVETGYFFIGQVLYTDTKTYAMGHLIQRKVH 218
 Db 125 -----TEVMWQPVLRGRGLEAAGQDIVRVMDTGIIYLLYSQVLFHDVFTFMGVVSRE--- 176
 QY 219 VFGDELSTLVTPRCIONMPELTPN---NSCYSAGIAKLEEGDELOLAIPRENAQISLDOD 275
 Db 177 ---GQRRETLFRCIISMPSD-PDRAYNSCYSANGVFLHQGDIIIVKIPRANKLSLSPH 232
 QY 276 VTFFGALKL 284
 Db 233 GTFLGFVKL 241
 RESULT 4
 TN13_HUMAN STANDARD; PRT; 250 AA.
 ID TN13_HUMAN Q96HV6; Q9P1M8; Q9P1M9;
 AC Q75888; Q96HV6; Q9P1M8; Q9P1M9;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor ligand superfamily member 13 (A proliferation-
 DE inducing ligand) (APRIL) (TNF-and APOL-related leukocyte expressed
 DE ligand 2) (TALL-2) (TNF-related death ligand-1) (TRDL-1).
 GN TNFSF13 OR APRIL OR TALL2 OR ZTNF2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Uterus;
 RX MEDLINE=98416181; PubMed=9743536;
 RA Hahne M., Kataoka T., Schroeter M., Hofmann K., Irmeler M.,
 RA Bodmer J.-L., Schneider P., Bornand T., Holler N., French L.E.,
 RA Sordat B., Rimoldi D., Tschopp J.;
 RT "APRIL, a new ligand of the tumor necrosis factor family, stimulates
 tumor cell growth.";
 RL J. Exp. Med. 188:1185-1190(1998).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99260341; PubMed=10331498;
 RA Shu H.-B., Hu W.-H., Johnson H.;
 RT "TALL-1 is a novel member of the TNF family that is down-regulated by
 mitogens.";
 RL J. Leukoc. Biol. 65:680-683(1999).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99260341; PubMed=10331498;
 RA Farrah T., Grant F., Haldeman B., Whitmore T., Gross J., O'Hara P.;
 RT "Homo sapiens tumor necrosis factor homolog.";
 RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 [4]
 RP SEQUENCE FROM N.A. (ISOFORMS ALPHA; BETA AND GAMMA).
 RX MEDLINE=20168636; PubMed=10706119;
 RA Kelly K.A., Manos E.J., Jensen G.T., Nadauld L., Jones D.A.;
 RT "APRIL/TRDL-1, a tumor necrosis factor-like ligand, stimulates cell
 death.";
 RL Cancer Res. 60:1021-1027(2000).
 [5]
 RP SEQUENCE OF 1-247 FROM N.A.
 RN SEQUENCE=Ovary;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [6]
RN FUNCTION.
RN MEDLINE=21170294; PubMed=10973284;
RX Yu G., Boone T., Delaney J., Hawkins N., Kelley M.J., Ramakrishnan M.,
RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
RA "APRIL and TALL-1 and receptors BCMA and TACI: system for regulating
RT humoral immunity";
RL Nat. Immunol. 1:252-256(2000).
RN [7]
RN PROCESSING BY FURIN, MUTAGENESIS OF ARG-101 AND ARG-104, AND
RP SUBCELLULAR LOCATION.
RX MEDLINE=21486098; PubMed=11571266;
RA Lopez-Fraga M., Fernandez R., Albar J.P., Hahne M.;
RT "Biologically active APRIL is secreted following intracellular
RT processing in the Golgi apparatus by furin convertase";
RL EMBO Rep. 2:945-951(2001).
CC -1- FUNCTION: Cytokine that binds to TNFRSF13B/TACI and to
CC TNFRSF17/BCMA. May be implicated in the regulation of tumor cell
CC growth. May be involved in monocyte/macrophage-mediated
CC immunologic processes.
CC -1- SUBUNIT: Homotrimer (Potential).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALTERNATIVE PRODUCTS:
CC Event-Alternative splicing; Named isoforms=3;
CC Name=Alpha;
CC IsoId=O75888-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=O75888-2; Sequence=VSP_006450;
CC Name=Gamma;
CC IsoId=O75888-3; Sequence=VSP_006451;
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN TRANSFORMED CELL
CC LINES, CANCERS OF COLON, THYROID, LYMPHOID TISSUES AND
CC SPECIFICALLY EXPRESSED IN MONOCYTES AND MACROPHAGES.
CC -1- INDUCTION: DOWN-REGULATED BY PHORBOL MYRISTATE ACETATE/IONOMYCIN
CC TREATMENT.
CC -1- PTM: The precursor is cleaved by furin.
CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
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CC -----
CC EMBL; AF046888; AAC61312.1; -;
CC EMBL; AF136294; AAD29422.1; -;
CC EMBL; AF184972; AAF01321.1; -;
CC EMBL; AF114011; AAF59828.1; -;
CC EMBL; AF114012; AAF59829.1; -;
CC EMBL; AF114013; AAF59830.1; -;
CC EMBL; BC008042; AAH08042.1; -;

DR Genew; HGNC:11928; TNFSF13.
DR MIM; 604472; -;
DR GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
DR GO; GO:0007165; P:signal transduction; TAS.
DR InterPro; IPR006052; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS0049; TNF_2; 1.
KW Cytokine; Immune response; Glycoprotein;
KW Alternative splicing.
FT PROPEP 1 104
FT CHAIN 105 250
FT SITE 104 105
FT DISULFID 196 211
FT CARBOHYD 124 124
FT VARSPLIC 113 129
FT VARSPLIC 247 249
FT MUTAGEN 101 104
FT CONFLICT 96 96
FT CONFLICT 247 247
SQ SEQUENCE 250 AA; 27433 MW; AE1AGB9457F6E298 CRC64;
Query Match 16.9%; Score 244.5; DB 1; Length 250;
Best Local Similarity 29.7%; Pred. No. 1.2e-13;
Matches 70; Conservative 47; Mismatches 90; Indels 29; Gaps 8;
QY 54 LALLSCCLTVVSYQVAALQGLASLRAELQGHAEKLPK--GAGAPKAGLEEAPVATG 111
Db 39 LGAVACAMALUT-----QQTELQSLRREVSRLQGTGGPSQNGEGYQWQLPEQS--SDA 90
QY 112 LKIFEPAPGEGNSNSNRKRAVQGPETVTQCLQLADSETPTTKGSGYTFVPWLLS 171
Db 91 LEAWE-----NGERSRKRRAVLTKQKQKQSVLHLVLPINAT--SKDDSDVTEVMQPA 141
QY 172 FKRGSALEKENKILVKETGYFFIVGVLYDKTYAMGHLLQKRVHGVFGDELSTVTLFR 231
Db 142 LRRGRGLQAGYGVRIQDAGVLYLSQVLFQDVTFTMGQVVSRE-----GQGRQETLFR 195
QY 232 CIQNMPETLPN---NSCYSAGIAKLEGEDELQLAIPRENAQISLDGVDVTFFGALKL 284
Db 196 CIRSMPSHPDRAYNSCYSAGVFLHOGDILSVIIPRAKLNLSPHGTFLGFKVL 250
RESULT 5
TNFA_CANFA
ID TNFA_CANFA STANDARD; PRT; 233 AA.
AC P51742; Q28339;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (TNF-a) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RT Fiers W.;
RT "Tumour necrosis factor.";
RL (In) Sim E. (eds.);
RL The natural immune system humoral factors, pp.65-119, IRL Press,
RL Oxford (1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Zucker K., Lu P., Fuller L., Asthana D., Esquenazi V., Miller J.;
RT "Cloning and expression of the cDNA for canine tumor necrosis

```

Db      32  CLSLFSLVLVAGATTLLFLHFGVIGPQRELP-----NGQLISPLA 74
QY      120  PGEENSSNRNK--RAYGPPETVTDCLQLIADSEPTIQKGSYTFVPWLLSPKRG 176
Db      75  QTVKSSRRPSPDPVAHVANPE-----AEGQ-----LQMD--SRRAN 110
QY      177  AL-----EKENKILYKETGYFFIYGQVLYTDKTYAMGHLIQRKVHVFG----DELSLV 227
Db      111  ALLANGVELTDNQLIIVSPDGLYLIYSQVLFKGGCPSTHVLLTHHTISREAVSVQTKVNL 170
QY      228  TLF--CIQMPETLNNSCYS-----AGIAKLEEGDELQIAPRENNQIISLQDDVTFGGA 281
Db      171  SAIKSPQCRTPETPEGTAKPWIEPIYLGGVFQLEKGRLSAEINLPYLDFAESGQYVFGI 230
QY      282  LKL 284
Db      231  IAL 233

RESULT 6
TNFA_TURTR
ID TNFA_TURTR STANDARD; PRT; 233 AA.
AC Q9BEA1;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (TNF-a) (cachectin).
DE TNF OR TNFSF2 OR TNFA.
OS Tursiops truncatus (Atlantic bottlenose dolphin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Tursiops.
OX NCBI_TaxID=9739;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21472839; PubMed=11587733;
RA Shoji Y., Inoue Y., Sugisawa H., Ito T., Endo T., Sakai T.;
RT "Molecular cloning and functional characterization of bottlenose
RT dolphin (Tursiops truncatus) tumor necrosis factor alpha.";
RL Vet. Immunol. Immunopathol. 82:183-192(2001).
CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation (By similarity).
CC -!- SUBUNIT: Homotrimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -!- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
-----
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-----
DR EMBL; AB049358; BAB39855.1; -
DR HSSP; P01375; 4TSV.
DR InterPro; IPR006053; TNF_ab.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF; 1.

```



```

Db 75 QTLRSSRTPKDPVAVHVPNPE-----AEQG-----LQWL--SRAN 110
QY 177 AL-----EKENKILKVGTFYIGQVLYTDKTYAMGHLIQKKVHVFQ-----DELSIV 227
Db 111 ALLANGVELTDNOLKVPISDGLYIYISQVLTGCGCPSTHVLTHTISRPAVSYQTKVNL 170
QY 228 TLFR--CIQNMPTLPNNSCYS-----AGIAKEEGDELQLAIPRENAQISLD---GDVT 277
Db 171 SAIKSPCQRETPEGAIAKWPYEPYLGGVFQLEKGDRLSTEL---NLPAYLDFAESQGV- 226
QY 278 FEGALKL 284
Db 227 YFGIIAL 233

```

RESULT 8

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TNFA_DELLE STANDARD; PRT; 233 AA.
AC QGWNRL; 2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (TNF-a) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OX NCBI_TaxID=5749;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21618234; PubMed=11768130;
RA Denis F., Archambault D.;
RT "Molecular cloning and characterization of beluga whale
RT (Delphinapterus leucas) interleukin-beta and tumor necrosis
RT factor-alpha.";
RL Can. J. Vet. Res. 65:233-240(2001).
CC -I- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation (By similarity).
CC -I- SUBUNIT: Homotrimer (By similarity).
CC -I- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form (By similarity).
CC -I- PTM: The soluble form derives from the membrane form by
CC proteolytic processing (By similarity).
CC -I- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -I- SIMILARITY: Belongs to the tumor necrosis factor family.
CC
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CC
CC EMBL; AF320323; AAL56946.1; .
CC InterPro: IPR006053; TNF.abc.
CC InterPro: IPR006052; TNF.family.
CC InterPro: IPR003636; TNF.subf.
CC Pfam: PF00229; TNF; 1.
CC PRINTS; PR01234; TNECROSISFCT.
CC ProDom; PD002012; TNF.subf; 1.
CC SMART; SM00207; TNF; 1.

```

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DR PROSITE; PS00251; TNF_1; 1.
KW PROSITE; PS00049; TNF_2; 1.
DR Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT CHAIN 78 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM.
FT DOMAIN 1 35 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 57 233 EXTRACELLULAR (POTENTIAL).
FT SITE 77 78 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CKI) (BY SIMILARITY).
FT DISULFID 145 177 BY SIMILARITY.
FT CARBOHYD 95 95 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 233 AA; 25420 MW; 2DF37DCB2BC9E61 CRC64;

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QY 120 PEGNSQNSNRKRAVGPEETVTDCLLIADSETPTIOKGSYTFVPWLLSPKR---GS 176
Db 75 QTLRSSKTSNK-----PVAHVYVANLSAQGQ-----LRWLNTYANTLLAN 115
QY 177 ALEKENKILKVGTFYIGQVLYTDKTYAMGHL-----IQKKVHVFGEDELSLTLFR 231
Db 116 SVKLEDNQLVPTDGLYIYISQVLFRCGCPSTHVLTHTISRIVAS-YOTKVNLSAIAK 174
QY 232 --CIQNMPTLP-----NNSCYSAGIAKLEEGDELQLAIPRENAQISL-----DGDVTF 278
Db 175 SPCQRETPEGAIAKWPYEPYLGGVFQLEKGDRL-----SAEINLPDYLDFAESQGV 227
QY 279 FEGALKL 284
Db 228 YFGIIAL 233

RESULT 9
TNFA_RAT STANDARD; PRT; 235 AA.
AC P16599; Q9J126; Q9J127;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE ligand superfamily member 2) (TNF-a) (Cachectin).
GN TNF OR TNFSF2 OR TNFA.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Shirai T., Shimizu N., Horiguchi S., Ito H.;
RT "Cloning and expression in Escherichia coli of the gene for rat tumor
RT necrosis factor.";
RL Agric. Biol. Chem. 53:1733-1736(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92329007; PubMed=1627266;
RA Estler H.C., Grewe M., Gaussling R., Pavlovic M., Decker K.;
RT "Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells
RT and in vitro posttranslational processing based on a PCR-derived
RT cDNA.";
RL Biol. Chem. Hoppe-Seyler 373:271-281(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=94040766; PubMed=8224868;
RA Kwon J., Chung I.Y., Benveniste E.N.;

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RT "Cloning and sequence analysis of the rat tumor necrosis
 RL factor-encoding genes.";
 RN Gene 132:227-236(1993).
 RP [4]
 RC SEQUENCE FROM N.A.
 RC STRAIN-ACI/SegHsd, BB(DR)/Wor, BN/SSNhd, DA/Bkl, F344/NHsd, and
 RC LEW/NHsd;
 RX MEDLINE=21369712; PubMed=11477479;
 RA Furuya T., Joe B., Salstrom J.L., Hashimoto A., Dobbins D.E.,
 RA Wilder R.L., Remmers E.F.;
 RT "Polymorphisms of the tumor necrosis factor alpha locus among
 RT autoimmune disease susceptible and resistant inbred rat strains.";
 RL Genes Immun. 2:229-232(2001).
 RP [5]
 RP SEQUENCE FROM N.A.
 RA Decker K.F.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RP [6]
 RP SEQUENCE FROM N.A., AND VARIANTS PRO-122 AND GLU-190.
 RC STRAIN-Dark Agouti;
 RC Seidel M.F., Junier M.-P., Vetter H.;
 RA "TNF-alpha polymorphism in rats with collagen-induced arthritis.";
 RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
 RL [7]
 RP SEQUENCE OF 1-231 FROM N.A.
 RC TISSUE-Tail;
 RA Kirisits M.J., Vardimon D., Kunz H.W., Gill T.J. III;
 RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC proin causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia. Under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation.
 CC -1- SUBUNIT: Homotrimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (By similarity).
 CC -1- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -1- PTM: The membrane form, but not the soluble form, is
 CC phosphorylated on serine residues. Dephosphorylation of the
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 CC similarity).
 CC -1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
 CC AND MALNUTRITION.
 CC -1- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -----
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 CC EMBL; AF330313; AAK53899.1; -
 CC EMBL; AF330314; AAK53900.1; -
 CC EMBL; AF330315; AAK53901.1; -
 CC EMBL; AF330316; AAK53902.1; -
 CC EMBL; AF330317; AAK53903.1; -
 CC EMBL; AF330318; AAK53904.1; -
 CC EMBL; AF330319; AAK53905.1; -
 CC EMBL; AF330320; AAK53906.1; -
 CC EMBL; AF330321; AAK53907.1; -
 CC EMBL; AF330322; AAK53908.1; -
 CC EMBL; AF330323; AAK53909.1; -
 CC EMBL; AF330324; AAK53910.1; -
 CC EMBL; AF330325; AAK53911.1; -
 CC EMBL; AF330326; AAK53912.1; -
 CC EMBL; AF330327; AAK53913.1; -
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 CC EMBL; AF330329; AAK53915.1; -
 CC EMBL; AF330330; AAK53916.1; -
 CC EMBL; AF330331; AAK53917.1; -
 CC EMBL; AF330332; AAK53918.1; -
 CC EMBL; AF330333; AAK53919.1; -
 CC EMBL; AF330334; AAK53920.1; -
 CC EMBL; AF330335; AAK53921.1; -
 CC EMBL; AF330336; AAK53922.1; -
 CC EMBL; AF330337; AAK53923.1; -
 CC EMBL; AF330338; AAK53924.1; -
 CC EMBL; AF330339; AAK53925.1; -
 CC EMBL; AF330340; AAK53926.1; -
 CC EMBL; AF330341; AAK53927.1; -
 CC EMBL; AF330342; AAK53928.1; -
 CC EMBL; AF330343; AAK53929.1; -
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 CC EMBL; AF330345; AAK53931.1; -
 CC EMBL; AF330346; AAK53932.1; -
 CC EMBL; AF330347; AAK53933.1; -
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 CC EMBL; AF330353; AAK53939.1; -
 CC EMBL; AF330354; AAK53940.1; -
 CC EMBL; AF330355; AAK53941.1; -
 CC EMBL; AF330356; AAK53942.1; -
 CC EMBL; AF330357; AAK53943.1; -
 CC EMBL; AF330358; AAK53944.1; -
 CC EMBL; AF330359; AAK53945.1; -
 CC EMBL; AF330360; AAK53946.1; -
 CC EMBL; AF330361; AAK53947.1; -
 CC E

RP SEQUENCE FROM N.A.
RX MEDLINE-85298296; PubMed-3898078;
RA Pennica D., Hayflick J.S., Bringman T.S., Palladino M.A.,
RA Goeddel D.V.;
RT "Cloning and expression in Escherichia coli of the cDNA for murine
RT tumor necrosis factor.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:6060-6064(1985).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-86149365; PubMed-2419912;
RA Caput D., Beutler B., Hartog K., Thayer R., Brown-Shimer S.,
RA Cerami A.;
RT "Identification of a common nucleotide sequence in the
RT 3'-untranslated region of mRNA molecules specifying inflammatory
RT mediators.";
RL Proc. Natl. Acad. Sci. U.S.A. 83:1670-1674(1986).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE-85242112; PubMed-2989794;
RA Fransen L., Mueller R., Marmenout A., Tavernier J., van der Heyden J.,
RA Kawashima E., Chollet A., Tizard R., van Heuverswyn H., van Vliet A.,
RA Ruysschaert M.-R., Piers W.;
RT "Molecular cloning of mouse tumour necrosis factor cDNA and its
RT eukaryotic expression.";
RL Nucleic Acids Res. 13:4417-4429(1985).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE-87298639; PubMed-3040015;
RA Shakhov A.N., Nedospasov S.A.;
RT "Molecular cloning of genes coding for tumor necrosis factor.
RT Complete nucleotide sequence of the genome copy of TNF-alpha in
RT mice.";
RL Bioorg. Khim. 13:701-705(1987).
RN [6]
RP SEQUENCE FROM N.A.
RX MEDLINE-88067722; PubMed-3684584;
RA Semon D., Kawashima E., Jongeneel C.V., Shakhov A.N., Nedospasov S.A.;
RT "Nucleotide sequence of the murine TNF locus, including the TNF-alpha
RT (tumor necrosis factor) and TNF-beta (lymphotoxin) genes.";
RL Nucleic Acids Res. 15:9083-9084(1987).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN-CTS, and NOD;
RX MEDLINE-96013654; PubMed-7560085;
RA Ikegami H., Makino S., Yamato E., Kawaguchi Y., Ueda H., Sakamoto T.,
RA Takekawa K., Ogihara T.;
RT "Identification of a new susceptibility locus for insulin-dependent
RT diabetes mellitus by ancestral haplotype congenic mapping.";
RL J. Clin. Invest. 96:1936-1942(1995).
RN [8]
RP SEQUENCE FROM N.A., AND VARIANTS THR-7 AND ALA-77.
RC STRAIN-A/J, BALB/c, and C57BL/6;
RX MEDLINE-97246744; PubMed-9089109;
RA Iraqi F., Teale A.;
RT "Cloning and sequencing of the Tnfa genes of three inbred mouse
RT strains.";
RL Immunogenetics 45:459-461(1997).
RN [9]
RP SEQUENCE FROM N.A.
RA Rowen L., Qin S., Madan A., Abbasi N., James R., Dickhoff R.,
RA Shaffer T., Ratcliffe A., Loretz C., Lasky S., Hood L.;
RT "Sequence of the mouse major histocompatibility class III region.";
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [10]
RP SEQUENCE OF 1-96 FROM N.A.
RC STRAIN-BLG2/Msf, BFM/2Msf, C57BL/10SnJ, CAST/EI, MSM/Msf,
RC NUL/Msf, pgn2, and SWN/Msf;
RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriaki K., Saitou N.;
RT "Conspicuous differences among gene genealogies of 21 nuclear genes of
RT five Mus musculus subspecies.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [11]
RP SEQUENCE OF 70-87.
RX MEDLINE-89380231; PubMed-2777790;
RA Cseh K., Beutler B.;
RT "Alternative cleavage of the cachectin/tumor necrosis factor
RT propeptide results in a larger, inactive form of secreted protein.";
RL J. Biol. Chem. 264:16256-16260(1989).
RN [12]
RP SEQUENCE OF 80-99.
RX MEDLINE-91097531; PubMed-2268312;
RA Sherry B., Juc D.-M., Zentella A., Cerami A.;
RT "Characterization of high molecular weight glycosylated forms of
RT murine tumor necrosis factor.";
RL Biochem. Biophys. Res. Commun. 173:1072-1078(1990).
RN [13]
RP IDENTIFICATION OF MEMBRANE-BOUND FORM.
RX MEDLINE-88165056; PubMed-3349526;
RA Krieger M., Perez X., Defay K., Albert I., Lu S.D.;
RT "A novel form of TNF/cachectin is a cell surface cytotoxic
RT transmembrane protein: ramifications for the complex physiology of
RT TNF.";
RL Cell 53:45-53(1988).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS) OF 80-235.
RX MEDLINE-99190964; PubMed-10089307;
RA Baeyens K.J., De Bondt H.L., Raeymaekers A., Fiers W., De Ranter C.J.;
RT "The structure of mouse tumour-necrosis factor at 1.4 A resolution:
RT towards modulation of its selectivity and trimerization.";
RL Acta Crystallogr. D 55:772-778(1999).
CC -I- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can
CC induce cell death of certain tumor cell lines. It is potent
CC pyrogen causing fever by direct action or by stimulation of
CC interleukin 1 secretion and is implicated in the induction of
CC cachexia. Under certain conditions it can stimulate cell
CC proliferation and induce cell differentiation.
CC -I- SUBUNIT: Homotrimer.
CC -I- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC extracellular soluble form.
CC -I- PTM: The soluble form derives from the membrane form by
CC proteolytic processing.
CC -I- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -I- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -I- SIMILARITY: Belongs to the tumor necrosis factor family.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M20155; AAA0462.1; ALT_SEQ.
CC EMBL; M11731; AAA0458.1; -
CC EMBL; M13049; AAA0457.1; -
CC EMBL; X02611; CAA26457.1; -
CC EMBL; M38296; AAA0459.1; -
CC EMBL; Y00467; CAA68530.1; -
CC EMBL; U06950; AAA18594.1; -
CC EMBL; M84196; BAA19512.1; -
CC EMBL; M84194; BAA19512.1; JOINED.
CC EMBL; M84195; BAA19512.1; JOINED.
CC EMBL; M84199; BAA19513.1; -
CC EMBL; M84197; BAA19513.1; JOINED.
CC EMBL; M84198; BAA19513.1; JOINED.
CC EMBL; U68414; AAB5593.1; -
CC EMBL; AF109719; AAC82484.1; -
CC EMBL; AB039224; BAB68748.1; ALT_SEQ.
CC EMBL; AB039225; BAB68749.1; ALT_SEQ.

Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
[1]
SEQUENCE FROM N.A.
MEDLINE=94083525; PubMed=8260599;
Cluets I., Cleuter Y., Kettmann R., Burny A., Droogmans L.;
"Cloning and characterization of the tandemly arranged bovine
lymphotoxin and tumour necrosis factor-alpha genes.";
Cytokine 5:336-341(1993).
[2]
SEQUENCE FROM N.A.
STRAIN=Boran, and N'Dama;
Iraqi F.;
"Bovine TNF-alpha gene.";
Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
Ahn J.;
Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE OF 50-233 FROM N.A.
TISSUE=Blood;
MEDLINE=96006582; PubMed=7590981;
Martens B.E.L.C., Muriuki M., Gaidulis L.;
"Cloning of two members of the TNF-superfamily in cattle: CD40 ligand
and tumor necrosis factor alpha.";
Immunogenetics 42:430-431(1995).
[5]
SEQUENCE OF 89-193 FROM N.A.
STRAIN=Holstein;
PubMed=9303477;
Dietz A.B., Nelbergs H.L., Womack J.E., Kehrl M.E., Jr.;
"Rapid communication: single strand conformational polymorphism (SSCP)
of bovine tumor necrosis factor alpha.";
J. Anim. Sci. 75:2567-2567(1997).
-1- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
induce cell death of certain tumor cell lines. It is potent
pyrogen causing fever by direct action or by stimulation of
interleukin 1 secretion and is implicated in the induction of
cachexia. Under certain conditions it can stimulate cell
proliferation and induce cell differentiation.
-1- SUBUNIT: Homotrimer (By similarity).
-1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
extracellular soluble form (By similarity).
-1- PTM: The soluble form derives from the membrane form by
proteolytic processing (By similarity).
-1- PTM: The membrane form, but not the soluble form, is
phosphorylated on serine residues. Dephosphorylation of the
membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
similarity).
-1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
AND MALNUTRITION.
-1- SIMILARITY: Belongs to the tumor necrosis factor family.

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or send an email to license@isb-sib.ch).

EMBL: Z14137; CAAT78511.1; -
EMBL: AF011926; AAB84086.1; -
EMBL: AF348421; AAN76506.1; -
EMBL: AF011927; AAB84087.1; -
EMBL: Z48808; CAA88743.1; -
EMBL: U11040; AAA19573.1; ALT_SEQ.
PIR: I46047; S24642.
HSP: P01375; 4T5V.
InterPro: IPR006053; TNF_ab0.


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Db          | : |
            231 GVIAL 235

RESULT 13
TNFA_PIG
ID  TNFA_PIG      STANDARD;      PRT;      232 AA.
AC  P23563;
DT  01-NOV-1991 (Rel. 20, Created)
DT  01-NOV-1991 (Rel. 20, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
GN  ligand superfamily member 2) (TNF-a) (Cachectin).
OS  TNF OR TNFSF2 OR TNFA.
OS  Sus scrofa (Pig).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX  NCBI_TaxID=9823;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=91016861; PubMed=2216741;
RA  Drews R.T., Coffee B.W., Prestwood A.K., McGraw R.A.;
RT  "Gene sequence of porcine tumor necrosis factor alpha.";
RL  Nucleic Acids Res. 18:5564-5564(1990).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  TISSUE=Liver;
RA  MEDLINE=91340150; PubMed=1874444;
RA  Kuhnert P., Wuethrich C., Peterhans E., Pauli U.;
RT  "The porcine tumor necrosis factor-encoding genes: sequence and
RT  comparative analysis.";
RL  Gene 102:171-178(1991).
RN  [3]
RP  SEQUENCE FROM N.A.
RX  TISSUE=Macrophage;
RA  Choi C.S., Mollitor T.W., Lin G.F., Murtaugh M.P.;
RT  "Complete nucleotide sequence of a cDNA encoding porcine tumor
RL  necrosis factor-alpha.";
RA  Anim. Biotechnol. 2:97-105(1991).
RN  [4]
RP  SEQUENCE FROM N.A.
RX  STRAIN=Large white; TISSUE=Fibroblast;
RA  MEDLINE=21108615; PubMed=1169259;
RA  Chardon P., Rogel-Gallard C., Cattolico L., Duprat S., Vaiman M.,
RA  Renard C.;
RT  "Sequence of the swine major histocompatibility complex region
RT  containing all non-classical class I genes.";
RL  Tissue Antigens 57:55-65(2001).
RN  [5]
RP  SEQUENCE OF 44-232 FROM N.A.
RX  MEDLINE=90034181; PubMed=2478420;
RA  Pauli U., Beutler B., Peterhans E.;
RT  "Porcine tumor necrosis factor alpha: cloning with the polymerase
RT  chain reaction and determination of the nucleotide sequence.";
RL  Gene 81:185-191(1989).
CC  -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC  TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
CC  induce cell death of certain tumor cell lines. It is potent
CC  pyrogen causing fever by direct action or by stimulation of
CC  interleukin 1 secretion and is implicated in the induction of
CC  cachexia, under certain conditions it can stimulate cell
CC  proliferation and induce cell differentiation.
CC  -!- SUBUNIT: Homotrimer (By similarity).
CC  -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC  extracellular soluble form (By similarity).
CC  -!- PTM: The soluble form derives from the membrane form by
CC  proteolytic processing (By similarity).
CC  -!- PTM: The membrane form, but not the soluble form, is
CC  phosphorylated on serine residues. Dephosphorylation of the
CC  membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (by
CC  similarity).
CC  -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC  CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH

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CC  AND MALNUTRITION
CC  -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC  -----
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CC  between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; X54001; CAA37949.1; -
DR  EMBL; X54859; CAA38639.1; -
DR  EMBL; X57321; CAA40591.1; -
DR  EMBL; AJ251914; CAB63852.1; -
DR  EMBL; M29079; AAA31128.1; -
DR  PIR; S12606; S12606.
DR  HSP; P01375; 4TSV.
DR  InterPro; IPR006053; TNF_abc.
DR  InterPro; IPR006052; TNF_family.
DR  InterPro; IPR003636; TNF_subf.
DR  Pfam; PF00229; TNF; 1.
DR  PRINTS; PR01234; TNECROSISFCT.
DR  ProDom; PD002012; TNF_subf; 1.
DR  SMART; SM00207; TNF; 1.
DR  PROSITE; PS00251; TNF_1; 1.
DR  PROSITE; PS00049; TNF_2; 1.
KW  Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT  CHAIN 1 232
FT  TUMOR NECROSIS FACTOR, MEMBRANE FORM.
FT  DOMAIN 77 232
FT  CYTOPLASMIC (POTENTIAL).
FT  SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT  TRANSMEM 36 56
FT  (POTENTIAL).
FT  DOMAIN 57 232
FT  SITE 76 77
FT  CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT  MOD_RES 2 2
FT  PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT  DISULFID 144 176
FT  BY SIMILARITY.
SQ  SEQUENCE 232 AA; 25254 MW; 65B28F702D99C8BE CRC64;

Query Match 7.4%; Score 107; DB 1; Length 232;
Best Local Similarity 22.0%; Pred. No. 0.057;
Matches 54; Conservative 40; Mismatches 86; Indels 66; Gaps 11;

QY 60 CLTVSVFYQVAALQGLDASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEP 119
   ||: || || || || || || || || || || || || || || || || || ||
Db 32 CLSFLVLLVAGATLFCLLHFEVIGPQKEFPAGP-----LSI-NPLA 74

QY 120 PEGNSSQNSRNKRAVGPEETVTQDCICLIADSETPTIQKSYTFVPWLLSFKR--GS 176
   | : || | : | : | : | : | : | : | : | : | : | : | : | : |
Db 75 QGLRSSQTS-----DKPVAHVAVNKAEGQ-----LQWQSGYANALLAN 114

QY 177 ALEKENKILVKETGYFFIYQVLYTDK-----TYAMGHLIQKKVHVFDELSLVTLFR 231
   : : ||: || : || || | : | : | : | : | : | : | : | : | : | :
Db 115 GVKLKDQLVVPVTDGLYLIYSQVLFRCGQCPSTNVFLTHTSIRAVS-YQTKVNLLSAIK 173

QY 232 --CTQNNPETLPNNSCYS----AGIAKLEGEDELQLAIPRENAQISL-----DGVTF 278
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Db 174 SPQRETPEGAEAKPWYEPIYLVGVFOLEKDDRL-----SAEINLPDYLDFAESQVY 226

QY 279 FGALKL 284
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Db 227 FGIAL 232

RESULT 14
TNFA_CAPHI
ID  TNFA_CAPHI      STANDARD;      PRT;      234 AA.
AC  P13296; Q28320; Q9MYZ2;
DT  01-JAN-1990 (Rel. 13, Created)
DT  28-FEB-2003 (Rel. 41, Last sequence update)
DT  15-SEP-2003 (Rel. 42, Last annotation update)
DE  Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE  ligand superfamily member 2) (TNF-a) (Cachectin).

```

GN TNF OR TNFSF2 OR TNFA.
 OS Capra hircus (Goat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Capra.
 OX NCBI_TaxID=9925;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleenocyte;
 RA Takakura H., Mori Y., Tatsumi M.;
 RT "Molecular cloning of caprine TNF-alpha cDNA and its expression in
 RL E.coli and insect cells.";
 RN Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 41-234 FROM N.A.
 RA Goldstein I.M., Henner D., Talhouk A.;
 RL Submitted (MAR-1989) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 44-234 FROM N.A.
 RC TISSUE=Ovarian follicle;
 RA Wang B., Zhang Y.;
 RT "Goat ovarian TNF alpha cDNA sequence.";
 RN Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 75-234 FROM N.A.
 RC TISSUE=Blood;
 RA Rimstad E.;
 RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia. Under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation.
 CC -!- SUBUNIT: Homotrimer (By similarity).
 CC -!- SURCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (By similarity).
 CC -!- PTM: The soluble form derives from the membrane form by
 CC proteolytic processing (By similarity).
 CC -!- PTM: The membrane form, but not the soluble form, is
 CC phosphorylated on serine residues. Dephosphorylation of the
 CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
 CC similarity).
 CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
 CC AND MALNUTRITION.
 CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
 CC -!- CAUTION: Ref.2 sequence differs from that shown due to a
 CC frameshift in position 60.
 CC -----
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 CC -----
 DR EMBL; D86587; BAA13130.1;
 DR EMBL; X14828; CAA32937.1; ALT_FRAME.
 DR EMBL; AF276985; AAF87741.1;
 DR EMBL; X77317; CAA54523.1;
 DR HSSP; P01375; 4TSV.
 DR InterPro; IPR006053; TNF_abc.
 DR InterPro; IPR006052; TNF_family.
 DR InterPro; IPR003636; TNF_subf.
 DR Pfam; PF00229; TNF; 1.
 DR PRINTS; PR01234; TNCRSISPT.
 DR ProDom; PD002012; TNF_subf; 1.
 DR SMART; SM00207; TNF; 1.
 DR PROSITE; PS00251; TNF_1; 1.
 DR PROSITE; PS50049; TNF_2; 1.

KW Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
 FT CHAIN 1 234
 FT CHAIN 79 234
 FT DOMAIN 1 35
 FT TRANSMEM 36 56
 FT DOMAIN 57 233
 FT MOD_RES 2 2
 FT SITE 78 79
 FT DISULFID 146 178
 FT CARBOHYD 96 96
 FT CONFLICT 79 79
 FT CONFLICT 119 119
 FT CONFLICT 129 129
 FT CONFLICT 155 155
 FT CONFLICT 164 164
 FT CONFLICT 184 184
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 FT CONFLICT 215 215
 FT SEQUENCE 234 AA; 25519 MW; 9768E33BBAB041 CRC64;
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 Query Match 7.3%; Score 106.5; DB 1; Length 234;
 Best Local Similarity 22.2%; Pred. No. 0.064;
 Matches 53; Conservative 37; Mismatches 104; Indels 45; Gaps 9;
 QY 58 SC-CLTVVSFYQVAALQGLDLSRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFE 116
 DB 29 SCWLSLFSLLVAGATTFLCULHFGVIGPQRE-----EUSP---AGPSNR 72
 QY 117 PPAPGSGNSQSNRKNRAVQGPETVTQDCLQIADSETPTIQKSYTFVPWLLSFKRGS 176
 DB 73 PLVQTLRSSQSSQSSNNKPA-----HVNANISAP-----QQLRWGDSYANALKAN 116
 QY 177 ALEKENKILVKETGYFFIYGVLY-----TKTAMGHILQKRVHVFVGDLSLVTLER 231
 DB 117 GVLEKDNQLVPTDGLYLIYSQVLFERHGCPTPLFTHTSIRIAVS-YQTKVNLSIAIK 175
 QY 232 --CIQNMPTFLP-----NNSCYSAGIAKLEEGDELQAIIPRENAQISLDGDTVFFGAKL 284
 DB 176 SPCHRTPEGAENKWPVEIYQGGVFOLEKGRLSNAEQPYLDYAESGQVYFGIAL 234
 RESULT 15
 TNFA_LAMGL STANDARD; PRT; 233 AA.
 AC PS9694; 2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
 DE ligand superfamily member 2) (TNF-a) (Cachectin).
 GN TNF OR TNFSF2 OR TNFA.
 OS Lama glama (Llama).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Tylopoda; Camelidae; Lama.
 OX NCBI_TaxID=9844;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Raadani O., Lee S., Yoshida R., Chang K., Ohashi K., Sugimoto C.,
 RA Onuma M.;
 RT "Cloning and sequence analysis of cytokine cDNAs of llama and camel.";
 RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
 CC TNFRSF1B/TNFR. It is mainly secreted by macrophages and can
 CC induce cell death of certain tumor cell lines. It is potent
 CC pyrogen causing fever by direct action or by stimulation of
 CC interleukin 1 secretion and is implicated in the induction of
 CC cachexia. Under certain conditions it can stimulate cell
 CC proliferation and induce cell differentiation (By similarity).
 CC -!- SUBUNIT: Homotrimer (By similarity).
 CC -!- SURCELLULAR LOCATION: Type II membrane protein. Also exists as an
 CC extracellular soluble form (By similarity).
 CC -!- PTM: The soluble form derives from the membrane form by

```
CC proteolytic processing (By similarity).
CC -!- PTM: The membrane form, but not the soluble form, is
CC phosphorylated on serine residues. Dephosphorylation of the
CC membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC similarity).
CC -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB107646; BAC75383.1; -
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Transmembrane; Signal-anchor; Phosphorylation.
FT CHAIN 1 233 TUMOR NECROSIS FACTOR, MEMBRANE FORM (BY
FT SIMILARITY).
FT CHAIN 77 233 TUMOR NECROSIS FACTOR, SOLUBLE FORM (BY
FT SIMILARITY).
FT DOMAIN 1 34 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 35 57 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (BY SIMILARITY).
FT DOMAIN 58 233 EXTRACELLULAR (POTENTIAL).
FT MOD_RES 2 2 PHOSPHORYLATION (BY CK1) (BY SIMILARITY).
FT SITE 76 77 CLEAVAGE (BY ADAM17) (BY SIMILARITY).
FT DISULFID 145 177 BY SIMILARITY.
SQ SEQUENCE 233 AA; 25437 MW; F5C07837505FBD86 CRC64;
```

Query Match 7.38; Score 105.5; DB 1; Length 233;
Best Local Similarity 22.28; Pred. No. 0.077;
Matches 53; Conservative 34; Mismatches 101; Indels 51; Caps 8;

```
Oy 60 CLTVVSYQVAALQGDLSLAELQGHAEKLPAGAPKAGLEAPAVTAGLKIFEPPA 119
Db 32 CLSLFLLVAGATTLECLLHFGVIGPQKEEL-----LTGLQIMNPLA 74
Oy 120 PGEGNSSQNRKRAVGQPEETVTQDCLQIADSETPTIQKSYTFVPWLLSFKR---GS 176
Db 75 QTLRSSQASRDKPVAHVADPAAGQLQ-----NEKREANTLLAN 115
Oy 177 ALEKENKILVKETGYFFIYGVLYTDK-----TYAMGHLIQKKVHVFGDELSLVTFR 231
Db 116 GVKLEDNQLVVPDGLYLYSQVLFSGQRCPTPVFLTHTISRLAYS-YPNKANLLSAIK 174
Oy 232 --C---IQNMPETILP-NNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDTVFFGALK 284
Db 175 SPCGGTSEAEAKPWYEPIYLGVTQLEKDRDLRAEINMPNYLDFAESGVYFGIAL 233
```

Search completed: August 28, 2003, 18:03:55
Job time : 24 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

QM protein - protein search, using sw model

Run on: August 28, 2003, 18:00:21 : Search time 97 seconds

(without alignments)
758.196 Million cell updates/sec

Title: US-09-507-968D-2

Perfect score: 1451

Sequence: 1 MDDSTEREQSLTCLCKRE.....ENAIQLDGDVTFFGALKLL 285

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_nhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1069	73.7	208	4	Q8IZI6
2	897	61.8	174	4	Q8IZI5
3	862.5	59.4	258	11	Q8BZM8
4	812	56.0	158	4	Q8IZI4
5	708	48.8	288	13	Q8JHJ4
6	339	23.4	199	11	Q8BWP2
7	336	23.2	194	11	Q8BVA3
8	247.5	17.1	410	11	Q8BX52
9	244.5	16.9	250	4	Q8NFH7
10	235.5	16.2	330	4	Q8IZK7
11	112.5	7.8	235	11	Q9JIT6
12	110.5	7.6	235	11	Q9JIT7
13	109	7.5	261	5	Q8MRW2
14	109	7.5	325	5	Q9V5G2
15	109	7.5	415	5	Q8MUJ1
16	106.5	7.3	252	11	Q8K3Y8

17	104.5	7.2	255	13	Q9DEP9	Q9dep9 oncorhynchu
18	102	7.0	287	13	Q90WT9	Q90wt9 gallus gall
19	102	7.0	409	5	Q8MY88	Q8my88 drosophila
20	101	7.0	409	5	Q8IGD3	Q8igd3 drosophila
21	100.5	6.9	205	4	Q8N4C3	Q8n4c3 homo sapien
22	99.5	6.9	217	6	Q8BEF4	Q8bef4 cabassous u
23	99	6.8	251	4	Q8NFE9	Q8nfe9 homo sapien
24	98	6.8	255	13	Q9I8I0	Q9i8i0 salvelinus
25	97.5	6.7	1596	13	Q9I8E1	Q9i8e1 fugu rubrip
26	97	6.7	217	11	Q9ERG6	Q9erg6 peromyscus
27	95.5	6.6	233	6	Q8MKG8	Q8mkg8 salmali sci
28	95.5	6.6	252	11	Q8K3Y7	Q8k3y7 rattus norv
29	95	6.5	289	17	Q8TVG6	Q8tv66 methanopyru
30	94.5	6.5	215	11	Q9NND1	Q99nd1 tamiascluru
31	94.5	6.5	237	13	Q8AWC9	Q8awc9 cyprinus ca
32	94.5	6.5	246	13	Q9I976	Q9i976 oncorhynchu
33	94.5	6.5	246	13	Q9I970	Q9i970 oncorhynchu
34	94.5	6.5	347	16	Q9RXM2	Q9rxm2 deinococcus
35	94	6.5	1695	5	Q9NK53	Q9nk53 drosophila
36	94	6.5	1711	5	Q9VJL0	Q9vj10 drosophila
37	94	6.5	1883	4	Q9H2Y7	Q9h2y7 homo sapien
38	93.5	6.4	157	4	Q43647	Q43647 homo sapien
39	93.5	6.4	214	6	Q9BEF3	Q9bef3 didephis m
40	93	6.4	596	10	Q9C977	Q9c977 arabidopsis
41	92.5	6.4	149	6	Q97543	Q97543 aotus nancy
42	92.5	6.4	253	13	Q8JFG3	Q8jfg3 sparus aura
43	92	6.3	1695	5	Q9U9R5	Q9u9r5 drosophila
44	92	6.3	1711	5	Q9U9R4	Q9u9r4 drosophila
45	91.5	6.3	2027	13	Q8UW52	Q8uw52 fugu rubrip

ALIGNMENTS

RESULT 1

Q8IZI6 PRELIMINARY; PRT; 208 AA.

AC Q8IZI6;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE B-lymphocyte stimulator (Fragment).
GN TNFSF13B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Gao H., He F., Li R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AV129226; AAN08422.1;
FT NONTER 1
SQ SEQUENCE 208 AA; 22767 MW; EEA31D227033AA53 CRC64;

Query Match	73.7%;	Score 1069;	DB 4;	Length 208;
Best Local Similarity	99.5%;	Pred. No. 2e-93;		
Matches 207;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
QY	78	SLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPPAPGEGNSQNSRNRKAVOG	137	
Db	1	SLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPPAPGEGNSQNSRNRKAVOG	60	
QY	138	PREVTQDCLQIADSETTIQKSYTFVPWLLSKFRGSALKEKENILVKETGYFFIYG	197	
Db	61	PREVTQDCLQIADSETTIQKSYTFVPWLLSKFRGSALKEKENILVKETGYFFIYG	120	
QY	198	QVLYTDKTYAMGHLQTKKKVHVFGDELSLVTIFRCIONMPETLPNNNSCSAGIAKLEEGD	257	
Db	121	QVLYTDKTYAMGHLQTKKKVHVFGDELSLVTIFRCIONMPETLPNNNSCSAGIAKLEEGD	180	
QY	258	ELQLAIPRENAQISLDGDVTFFGALKLL	285	

```
Db 181 ELQITIPRENAQISLDGDTFFGALKLL 208

RESULT 2
Q81Z15
ID Q81Z15 PRELIMINARY; PRT; 174 AA.
AC Q81Z15;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE B-lymphocyte stimulator (Fragment).
GN TNFSF13B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA He F., Gao H., Li R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY129227; AAN08423.1; -
FT NON_TER 1
SQ SEQUENCE 174 AA; 19479 MW; 1AEBD4F2862EB3E0 CRC64;

Query Match 61.8%; Score 897; DB 4; Length 174;
Best Local Similarity 99.4%; Pred. No. 3.5e-77;
Matches 173; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 112 LKIFEPAPGEGNSSNSRNKRAVQGPETVTDCLQLIADSETPTIQKGSYTFVPWLLS 171
Db 1 LKIFEPAPGEGNSSNSRNKRAVQGPETVTDCLQLIADSETPTIQKGSYTFVPWLLS 60
QY 172 FKRGSALEKENKILVKETGYFFYQGVLYTDKTYAMGHLIQKVKHVHVGDELSLVTFLR 231
Db 61 FKRGSALEKENKILVKETGYFFYQGVLYTDKTYAMGHLIQKVKHVHVGDELSLVTFLR 120
QY 232 CIONMPETLPNNSCYSAGTAKLEEGDELQAIIPRENAQISLDGDTFFGALKLL 285
Db 121 CIONMPETLPNNSCYSAGTAKLEEGDELQAIIPRENAQISLDGDTFFGALKLL 174

RESULT 3
Q8B2M8
ID Q8B2M8 PRELIMINARY; PRT; 258 AA.
AC Q8B2M8;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE Tumor necrosis factor (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RA STRAIN=C57BL/6J; TISSUE=Diiencephalon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).";
DR EMBL; AK034121; BAC28593.1; -
FT NON_TER 1
SQ SEQUENCE 258 AA; 28604 MW; E6431FE93E782810 CRC64;

Query Match 59.4%; Score 862.5; DB 11; Length 258;
Best Local Similarity 65.0%; Pred. No. 1.2e-73;
Matches 173; Conservative 24; Mismatches 30; Indels 39; Gaps 2;

QY 51 TLLALLSCLTVSVFYQVAALQGLASLRAELQGHAEKLPAGAPKAGLEEAPAVTA 110
Db 1 TLLALLSSFTAMSLYQLAALQADLMNLRELQSYRGSAATPAAGAPE-----LTA 52

RESULT 4
Q81Z14
ID Q81Z14 PRELIMINARY; PRT; 158 AA.
AC Q81Z14;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE B-lymphocyte stimulator (Fragment).
GN TNFSF13B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA He F., Gao H., Li R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY129228; AAN08424.1; -
FT NON_TER 1
SQ SEQUENCE 158 AA; 17826 MW; 8346BCC0D333DCAB CRC64;

Query Match 56.0%; Score 812; DB 4; Length 158;
Best Local Similarity 99.4%; Pred. No. 3.7e-69;
Matches 157; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 128 NSRNKRAVQGPETVTDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEKENKILV 187
Db 1 NSRNKRAVQGPETVTDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSALEKENKILV 60
QY 188 KETGYFFYQGVLYTDKTYAMGHLIQKVKHVHVGDELSLVTFLRCIONMPETLPNNSCYS 247
Db 61 KETGYFFYQGVLYTDKTYAMGHLIQKVKHVHVGDELSLVTFLRCIONMPETLPNNSCYS 120
QY 248 AGIAKLEEGDELQAIIPRENAQISLDGDTFFGALKLL 285
Db 121 AGIAKLEEGDELQAIIPRENAQISLDGDTFFGALKLL 158

RESULT 5
Q8JHJ4
ID Q8JHJ4 PRELIMINARY; PRT; 288 AA.
AC Q8JHJ4;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE TNF family B cell activation factor.
GN BAFB.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RA Schneider K., Kolthow S., Schneider P., Goebel T., Kaspers B.,
```

Db	172	QLIADSDTPTIRKGS	186	: :
RESULT 7				
Q8BVA3				
ID	Q8BVA3	PRELIMINARY;	PRT;	194 AA.
AC	Q8BVA3;			
DT	01-MAR-2003	(TREMBLrel. 23, Created)		
DT	01-MAR-2003	(TREMBLrel. 23, Last sequence update)		
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)		
DE	Tumor necrosis factor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI_TaxID=10090;				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Urinary bladder;			
RX	MEDLINE=22354683; PubMed=12466851;			
RA	The FANTOM Consortium,			
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotation of			
RT	60,770 full-length cDNAs."			
RL	Nature 420:563-573(2002).			
DR	EMBL; AK079180; BAC37571.1; -.			
SQ	SEQUENCE 194 AA; 20961 MW; 85FCF3495B138377 CRC64;			
	Query Match	23.2%;	Score 336;	DB 11; Length 194;
	Best Local Similarity	43.1%;	Pred. No. 8.8e-24;	
	Matches	84; Conservative	23; Mismatches	46; Indels 42; Gaps 5
Qy	1	MDDSTER-EQSRLTSCLLKREMKCEVSIPLRKESPS-VRSSKDGKLIATLILALLS	58	: :
Db	1	MDESATLPPCLCFCEKGEDMKV-GYDPTTPQKEGANFGICRGRLLAATLILALLS	59	: :
Qy	59	CLLTVVSYFVQAALGDIALSRDELQGHAAKLPAGAGAPKAGLEAPAVTAGLKIFEP	118	: :
Db	60	SSTATMSLYQLAALQDLMLNLRMELQSYRGSATPAAAGAPE-----LTAGVKLLT	111	: :
Qy	119	APGEGNSSONSNRKRAVGPEET-----VTQDCL	147	: :
Db	112	APRPHNSSGHRNRARFQGPETEODVDLSAPPAPCLPGCRHSQHDDNGMNLRIIQDCL	171	: :
Qy	148	QLIADSDTPTIRKGS	162	: :
Db	172	QLIADSDTPTIRKGN	186	: :
RESULT 8				
Q8BXS2				
ID	Q8BXS2	PRELIMINARY;	PRT;	410 AA.
AC	Q8BXS2;			
DT	01-MAR-2003	(TREMBLrel. 23, Created)		
DT	01-MAR-2003	(TREMBLrel. 23, Last sequence update)		
DT	01-MAR-2003	(TREMBLrel. 23, Last annotation update)		
DE	Tumor necrosis factor.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
NCBI_TaxID=10090;				
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Retina;			
RX	MEDLINE=22354683; PubMed=12466851;			
RA	The FANTOM Consortium,			
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;			
RT	"Analysis of the mouse transcriptome based on functional annotation of			
RT	60,770 full-length cDNAs."			
RL	Nature 420:563-573(2002).			
DR	EMBL; AK044387; BAC31897.1; -.			
SQ	SEQUENCE 410 AA; 45881 MW; 590AE74C33FB8D4 CRC64;			

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Query Match      17.1%; Score 247.5; DB 11; Length 410;
Best Local Similarity 31.6%; Pred. No. 6.7e-15;
Matches 74; Conservative 35; Mismatches 78; Indels 47; Gaps 8;

Qy 68 QVAALQGQDILASRAELQGHAAEKLPAGAGAPKAG-----LEEAPVATGALKIFEPPAP 120
      | : | | | | | : : : | : | | | | | | | | | | | | | | | | | | | | |
Db 207 QLRLCQTELOSRLREV---SRLRSGGPGSQKGERPWSQSLWQSPDVLAWK----- 255
      | : | | | | | : : : | : | | | | | | | | | | | | | | | | | | | | |
Qy 121 GEGNSQSNRNKRRAVQGPPEETVODCQLI-----ADSETPTIQGSYTFVPWLLSFK 173
      | | | | | | : : : | : | | | | | | | | | | | | | | | | | | | | |
Db 256 ----DGAKSRRRRAVLTKHKHKSVLHLVPVNITSKADSDV-----TEVMQPVLR 303
      | | | | | | : : : | : | | | | | | | | | | | | | | | | | | | | |
Qy 174 RGSALAEENKILVKEICYFFLYGVLYTKDTYAMGHLTKQKKVHVFQGDLSLVTLFRCI 233
      | : | | | | : : : | : | | | | | | | | | | | | | | | | | | | | |
Db 304 RGRLEAGQDIVRWMDTGIIYLLLYSQVLFHDVTMTGQVVSRE-----GQGRRETLFRCI 357
      | : | | | | : : : | : | | | | | | | | | | | | | | | | | | | | |
Qy 234 QNMPETLPN---NSCYAGIAKLEEGDELQALAIPRENAQISLDGDVTFEGALKL 284
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 358 RSMPSD-PDRAYNSCYAGVPHLHGGDIIVKIPRANAKLSLSPHGTFLGFVKL 410
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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RESULT 9
Q8NFH7
ID Q8NFH7 PRELIMINARY; PRT; 250 AA.
AC Q8NFH7;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-NAR-2003 (TREMBLrel. 23, Last annotation update)
DE Proliferation-inducing ligand APRIL.
DE OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RX SEQUENCE FROM N.A.
RA Koyama T., Tsukamoto H., Masumoto K., Himeji D., Hayashi K.,
RA Harada M., Horiuchi T.;
RT "Genomic structure of APRIL, a proliferation-inducing ligand.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF513501; AAM47279.1; -.
DR InterPro; IPR006052; TNF_family.
DR Pfam; PF00229; TNF; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 250 AA; 27453 MW; AE1E4FDEDF578898 CRC64;

```

[illegible]

RESULT 10
Q81ZK7
ID Q81ZK7 PRELIMINARY; PRT; 330 AA.
AC Q81ZK7;
DT 01-MAR-2003 (TRENBLrel. 23, Created)

DT	01-MAR-2003	(TReMBUrel. 23, Last sequence update)
DT	01-MAR-2003	(TReMBUrel. 23, Last annotation update)
DE	TWE-PRIL.	
DE	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RP	MEDLINE=22299924; PubMed=12411489;	
RX	Prader-Balade B., Medema J.P., Lopez-Fraga M., Lozano J.C.,	
RA	Kollischoten G.M., Picard A., Martinez-A C., Garcia-Sanz J.A.,	
RA	Hahne M.	
RT	"An endogenous hybrid mRNA encodes TWE-PRIL, a functional cell surface	
RT	TWEAK-APRIL fusion protein."	
RL	EMBO J. 21:5711-5720(2002).	
RL	EMBL; AY081051; AAL90443.1; -.	
DR	SEQUENCE 330 AA; 36588 MW; FC673BCA29C029AE CRC64;	

Query Match	16.2%	Score 235.5;	DB 4;	Length 330;
Best Local Similarity	26.3%;	Pred. NO. 6,7e-14;		
Matches	73;	Conservative 45;	Mismatches 101;	Indels 59; Gaps 8;
QY	30	ILPKRSPSVRRSKDKLLAATLLALLSCLTWWFYQVAALQQGLASLRAELQGHAE	89	
		: : : : : : : : :		
Db	89	VPRRSAPKGRKTRARRATAA-----HYEVHPRGQ-----D	120	
QY	90	KLPAGAGAKPAGLEEAP-----AVTAGLKIF--EPPAPGEGNSQNS	129	
		: : : : : : : : :		
Db	121	GAAQGVDGTSGWEEEARINSSPLRYNRQIGETIVTRAGLYYYLCOSSDALEAWENGERS	180	
QY	130	RNKRAYQGPEETVTDQLLIADSETPTIQGSYTEFVPWLLSPKRGSALSEEKENKTILVE	189	
		: : : : : : : : :		
Db	181	RKRRAVLTKOKKHOSVHLHPVINAT-SKDSDSVTEVMQPALRRRGRLQAQCYGVRIQD	239	
QY	190	TGYFFYLGOVLYTDKYAMCHLTORKKVHVCGDELSLVTLFCIONNPETLPN---NSCY	246	
		: : : : : : : : :		
Db	240	AGVILYSQVLFDQVTFTMGVVVSRE-----CGRQETLFCIRSMPSHPDRAYNSCY	292	
QY	247	SAGIAKLEEGDELQOLAIPRENAQISLDGDVTFFGALKL	284	
Db	293	SAGVFHILHGODILSVIIPRARAKLNISPHTFGFVKL	330	

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RESULT 11
Q9JI26
ID Q9JI26 PRELIMINARY; PRT; 235 AA.
AC Q9JI26;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE TNF-alpha propeptide 3 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=Dark Agouti;
RA Seidel M.F., Junier M.-P., Vetter H.;
RT "TNF-alpha polymorphism in rats with collagen-induced arthritis.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AR269160; AAF82568.1; -
DR HSSP; P06804; 2TNF.
DR InterPro; IPR006053; TNF_abc.
DR InterPro; IPR006052; TNF_family.
DR InterPro; IPR003636; TNF_subf.
DR Pfam; PF00229; TNF_1.
DR PRINTS; PR01234; TNECROSISFCT.
DR ProDom; PD002012; TNF_subf; 1.
DR SMART; SM00207; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.

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FT   NON_TER      235          C801B92D049C2F2E CRC64;
SQ   SEQUENCE     235 AA;  25789 MW;  7.8%; Score 112.5; DB 11; Length 235;
Query Match
Best Local Similarity    22.2%; Pred. No. 0.02; Indels 57; Gaps 11;
Matches 54; Conservative 45; Mismatches 87; Indels 57; Gaps 11;

QY   60 CLTVVSYFYVAALOGDLASLRAELQG-HHAEKLPAGAGAPKAGLEAPAVTAGLKIFPEP 118
Db    |||: || |  | : | : | | | | | | | | | | | | | | | | | | | | | | | |
32 CLSLFSFLLVAGATTLCFLNFGVIGPNKEEPNG-----LPLISSMAQTTLTKR----- 81

QY   119 APGEGNSQNSNRKRAVGPEETVTQDCLQLIADSETPTIQKGSTFFYPWLLSKRGSA 178
Db    : ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
82 -----SSQNSSDRPVARHVANHQAEQLEWLQRANALLANG-----m 120

QY   179 EEKENILVKETGYFFIYGVLTYDK----TYAMGHLIOKKKHVHGDELSLVTLF--C 232
Db    : | : | : | : | | | | | : | : | : | : | : | : | : | : | : | : |
121 DPKNQNLVPADGLYLIIYSQVLFKGQCDDPYLLTHTVSFRFAIS-YQEKVSLLSAISKPC 179

QY   233 IQNMPEITLP-----NNSCYSAGIAKLEEGDELQLAIPRENAQISLDG--DVT-----PFGA 281
Db    :: || | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
180 PKDTPEGAEALPWPEMYLGIVGLEKGDLL-----SAEVNLPKYLDITESGOVFSGV 232

QY   282 LKL 284
Db    : |

QY   233 IAL 235

RESULT 12
Q9J127 PRELIMINARY; PRT; 235 AA.
ID Q9J127 AC
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DS TNF-alpha propeptide 5 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_Taxid=10116;
RX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Dark Agouti;
RA Seidel M.F., Junier M.-P., Vetter H.;
RL "TNF-alpha polymorphism in rats with collagen-induced arthritis.";
RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF265159; AAF82567.1; -
DR HSP: P06804; 2TNF.
DR InterPro: IPRO06053; TNF_abc.
DR InterPro: IPRO06052; TNF_family.
DR InterPro: IPRO03636; TNF_subf.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISPCT.
DR ProDom: PD002012; TNF_subf; 1.
DR SMART: SM00207; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS50049; TNF_2; 1.
DR NON_TER      235          C801B92D049C2F2E CRC64;
SQ   SEQUENCE     235 AA;  25806 MW;  7.6%; Score 110.5; DB 11; Length 235;
Query Match
Best Local Similarity    22.2%; Pred. No. 0.032; Indels 57; Gaps 11;
Matches 54; Conservative 45; Mismatches 87; Indels 57; Gaps 11;

QY   60 CLTVVSYFYVAALOGDLASLRAELQG-HHAEKLPAGAGAPKAGLEAPAVTAGLKIFPEP 118
Db    |||: || |  | : | : | | | | | | | | | | | | | | | | | | | | | | | |
32 CLSLFSFLLVAGATTLCFLNFGVIGPNKEEPNG-----LPLISSMAQTTLTKR----- 81

QY   119 APGEGNSQNSNRKRAVGPEETVTQDCLQLIADSETPTIQKGSTFFYPWLLSKRGSA 178
Db    : ||||| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
82 -----SSQNSSDRPVARHVANHQAEQLEWLQRANALLANG-----m 120

QY   179 EEKENILVKETGYFFIYGVLTYDK----TYAMGHLIOKKKHVHGDELSLVTLF--C 232
Db    : | : | : | : | | | | | : | : | : | : | : | : | : | : | : | : |
179 EEKENILVKETGYFFIYGVLTYDK----TYAMGHLIOKKKHVHGDELSLVTLF--C 232

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Db	121	DIKDNQVVPADGGLYLIYSQVLFKGGQCPDVLTHTVSRFAIS-YOEKVSLLSAIKSPC	179
QY	233	IGNMPTLP-----NNSCYSAGTAKLEGEDELQALAPRENAQISLDG--DVT-----FFGA	281
Db	180	PKDTPEGAELEPWPYEWTLGGVQLEKGDLL-----SAEVNLPKYLDITSGQVYFGV	232
QY	282	LKL 284	
Db	233	IAL 235	
RESULT 13			
ID	Q8MRW2	PRELIMINARY; PRT; 261 AA.	
AC	Q8MRW2;		
DT	01-OCT-2002 (TReMBLrel. 22, Created)		
DT	01-OCT-2002 (TReMBLrel. 22, Last sequence update)		
DT	01-MAR-2003 (TReMBLrel. 23, Last annotation update)		
DE	SD18286P.		
GN	EIGER OR CGI12919.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,		
RA	Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,		
RA	George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,		
RA	Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,		
RA	Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,		
RA	Celniker S.		
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY119233; AAM51093.1; -		
DR	FlyBase; FBgn0033483; eiger.		
DR	InterPro; IPR006052; TNF_family.		
DR	SMART; SM00207; TNF; 1.		
DR	PROSITE; PS00251; TNF.1; 1.		
DR	PROSITE; PS50049; TNF.2; 1.		
SQ	SEQUENCE 261 AA; 29780 MW; 13B6D5A04EC9122C CRC64;		
Query Match 7.5%; Score 109; DB 5; Length 261;			
Best Local Similarity 20.9%; Pred. No. 0.051;			
Matches 50; Conservative 44; Mismatches 79; Indels 66; Gaps 11			
QY	76	LASLRAE---LOGHHAELKLPACAGAPKAGLEAEPAVTAGLIKIFEPAPAGGNSQNSRNK	132
Db	59	IADVNRNEQIOGNHTE-----LOEKSSNEATSK--ESPAPLHRRRMHSRRH	104
QY	133	RAVQGPETVTQDLQIADSETPTIQGSYTFVPWLLSFKR--GSA-----	177
Db	105	HLIVRKGESL-----LSARSE-----DSRAAHFILSSRRRQSGNGYHGMVIGNDN	152
QY	178	-----LEEKENKILVKETGYFFIYQGVLYTDKTYAMGHLIQKKVHVFGDELVLTL	229
Db	153	ERNSYGHPQTRDGVLTNTGLYVYVYQAICYNNSHDQNGFIVFQ-----GD-----	202
QY	230	FRCIQNMPTLPN--NSCYSGIAGIKLEGEDELQALIPR--ENAIQLDGDVTFFGALKL	284
Db	203	LOCLNTVPTNMPKRVHTCHTSGLIHLERNRIHLKDHNDRNAVIREGNNRSYFGIFKV	261
RESULT 14			
QYV5G2	Q9V5G2	PRELIMINARY; PRT; 325 AA.	
AC	Q9V5G2;		
DT	01-MAY-2000 (TReMBLrel. 13, Created)		
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)		
DT	01-OCT-2002 (TReMBLrel. 22, Last annotation update)		
DE	CG12919 protein.		
GN	EIGER OR CGI12919.		

Db	121	DIKDNQVVPADGGLYLIYSQVLFKGGQCPDVLTHTVSRFAIS-YOEKVSLLSAIKSPC	179
QY	233	IGNMPTLP-----NNSCYSAGTAKLEGEDELQALAPRENAQISLDG--DVT-----FFGA	281
Db	180	PKDTPEGAELEPWPYEWTLGGVQLEKGDLL-----SAEVNLPKYLDITSGQVYFGV	232
QY	282	LKL 284	
Db	233	IAL 235	
RESULT 13			
ID	Q8MRW2	PRELIMINARY; PRT; 261 AA.	
AC	Q8MRW2;		
DT	01-OCT-2002 (TReMBLrel. 22, Created)		
DT	01-OCT-2002 (TReMBLrel. 22, Last sequence update)		
DT	01-MAR-2003 (TReMBLrel. 23, Last annotation update)		
DE	SD18286P.		
GN	EIGER OR CGI12919.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,		
RA	Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,		
RA	George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,		
RA	Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,		
RA	Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,		
RA	Celniker S.		
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AY119233; AAM51093.1; -		
DR	FlyBase; FBgn0033483; eiger.		
DR	InterPro; IPR006052; TNF_family.		
DR	SMART; SM00207; TNF; 1.		
DR	PROSITE; PS00251; TNF.1; 1.		
DR	PROSITE; PS00049; TNF.2; 1.		
SQ	SEQUENCE 261 AA; 29780 MW; 13B6D5A04EC9122C CRC64;		
Query Match 7.5%; Score 109; DB 5; Length 261;			
Best Local Similarity 20.9%; Pred. No. 0.051;			
Matches 50; Conservative 44; Mismatches 79; Indels 66; Gaps 11			
QY	76	LASLRAE---LOGHHAELKLPACAGAPKAGLEAEPAVTAGLIKIFEPAPAGGNSQNSRNK	132
Db	59	IADVRRNEEQIOGNHTE-----LOEKSSNEATSK--ESPAPLHRRRMRHSHR	104
QY	133	RAVQGPPEVTQDCLQIADSETPTIQGSYTFVPWLLSFKR--GSA-----	177
Db	105	HLIVRKGESL-----LSARSE-----DSRAAHFILSSRRRQGSNGYHGMVIGNDN	152
QY	178	-----LEEKENKILVKETGYFFIYQGVLYTDKTYAMGHLIQKKVHVFGDELVLTL	229
Db	153	ERNSYQGHQPTRDGVLTVNTGLYVYVYQAICYNNSHDQNGFIVFQ-----GD-----	202
QY	230	FRCIQNMPTLPN--NSCYSGIAGIKLEGEDELQALAPR--ENAIQLDGDVTFFGALK	284
Db	203	LOCLNTVPTNMPKRVHTCHTSGLIHLERNRIHLKDHNDRNAVIREGNNRSYFGIFKV	261
RESULT 14			
QYV5G2	Q9V5G2	PRELIMINARY; PRT; 325 AA.	
AC	Q9V5G2;		
DT	01-MAY-2000 (TReMBLrel. 13, Created)		
DT	01-MAY-2000 (TReMBLrel. 13, Last sequence update)		
DT	01-OCT-2002 (TReMBLrel. 22, Last annotation update)		
DE	CG12919 protein.		
GN	EIGER OR CGI12919.		

Search completed: August 28, 2003, 18:05:39
Job time : 98 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 17:53:21 ; Search time 86 seconds

(without alignments)
526.012 Million cell. updates/sec

Title: US-09-507-968D-2

Perfect score: 1451

Sequence: 1 MDDSTERQSLTCLKKRE.....ENAIQLDGDVTFGALKIL 285

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03:*

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- 2: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*
- 3: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
- 4: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
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- 23: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1451	100.0	285	19 AAW73043	Tumour necrosis fa
2	1451	100.0	285	19 AAW62461	Human T cell surfa
3	1451	100.0	285	19 AAW58391	Homo sapiens neutr
4	1451	100.0	285	20 AAY22221	Human TNF α protei
5	1451	100.0	285	20 AAY04392	Human Kay-ligand.
6	1451	100.0	285	20 AAW93586	Human TNF α -alpha
7	1451	100.0	285	21 AAB28553	Human TNF α Li. Homo
8	1451	100.0	285	21 AAB08659	Amino acid sequenc
9	1451	100.0	285	21 AAB08191	Amino acid sequenc

10	1451	100.0	285	21 AAB08261	Amino acid sequenc
11	1451	100.0	285	22 AAE09242	Human TALL-1 prote
12	1451	100.0	285	22 AAE07156	Human tumour necro
13	1451	100.0	285	22 AAE07879	Human BAFF protein
14	1451	100.0	285	22 AAY12183	Human PRO738 polyp
15	1451	100.0	285	22 AAY171915	Human TACI-ligand
16	1451	100.0	285	22 AAY19178	Human TNF and Apol
17	1451	100.0	285	23 AAE28963	Human TNF α protein
18	1451	100.0	285	23 ABG96458	Human Neurokine-a
19	1451	100.0	285	23 AAE26214	Human neurokine-a
20	1451	100.0	285	23 AAE24636	Human tumour necro
21	1451	100.0	285	23 ABH81485	Human TNF α amino
22	1451	100.0	285	23 ABJ00715	Human B lymphocyte
23	1451	100.0	285	23 ABP47217	Human Blys binding
24	1451	100.0	285	23 ABB95471	Human angiogenesis
25	1451	100.0	285	23 ABG33576	Human B lymphocyte
26	1451	100.0	285	23 ABG79140	Human Neurokine-a
27	1451	100.0	285	23 ABB90325	Human polypeptide
28	1451	100.0	285	23 ABB84865	Human PRO738 prote
29	1451	100.0	285	23 AAU75409	Neurokine-alpha (
30	1451	100.0	285	23 AAU10942	Human AGP-3. Homo
31	1451	100.0	285	24 ABU66581	Human PRO polypept
32	1451	100.0	285	24 ABU66857	Human secreted/tri
33	1451	100.0	285	24 AAE35212	Human tumour necro
34	1451	100.0	285	24 ABP97718	Amino acid sequenc
35	1451	100.0	285	24 ABU59662	Novel secreted and
36	1451	100.0	285	24 ABP57103	Membrane bound Bly
37	1451	100.0	285	24 ABP60543	Human tumour necro
38	1444	99.5	285	21 ABY97037	Membrane bound hum
39	1345	92.7	264	20 AAW82268	Human NTN-2 protei
40	1345	92.7	264	20 AAW82270	Human NTN-2 DNA se
41	1345	92.7	264	21 AAY94005	A human ztnf4, a t
42	1335.5	92.0	266	19 AAW62462	Human T cell surfa
43	1335.5	92.0	266	21 AAB08660	A human neurokine
44	1335.5	92.0	266	23 ABG96463	Human Neurokine-a
45	1335.5	92.0	266	23 AAE26215	Human neurokine-a

ALIGNMENTS

RESULT 1
AAW73043
ID AAW73043 standard; Protein; 285 AA.

XX AC AAW73043;

XX DT 07-JAN-1999 (first entry)

XX DE Tumour necrosis factor homologue TL5 protein.

XX DE Tumour necrosis factor homologue TL5; vaccine; chronic;
KW acute inflammation; arthritis; septicemia; autoimmune disease;
KW inflammatory bowel disease; psoriasis; transplant rejection;
KW graft vs. host disease; infection; stroke; ischaemia;
KW acute respirator disease syndrome; restenosis; brain injury; AIDS;
KW bone disease; cancer; lymphoproliferative disorder; atherosclerosis;
KW Alzheimer's disease.

XX OS Homo sapiens.

XX PN EP869180-A1.

XX PD 07-OCT-1998.

XX PF 01-APR-1998; 98EP-0302526.

XX PR 03-DEC-1997; 97US-0984396.

XX PR 02-APR-1997; 97US-0041797.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.

XX PI Hurle MR, Young PR;

```

XX WPI; 1998-508494/44.
DR N-PSDB; AAV58894.
XX
PT New tumour necrosis factor homologue, TL5 - useful for diagnosis and
PT treatment of Alzheimer's disease, AIDS and cancer
XX
XX Claim 10; Page 18; 23pp; English.
XX
CC The present sequence encodes a tumour necrosis factor homologue TL5
CC polypeptide sequence. TL5 polypeptides and antibodies are useful for
CC identifying compounds which agonise and antagonise TL5, and these can be
CC administered for treatment to inhibit TL5 activity (antagonist) or
CC enhance TL5 activity (agonist). Gene therapy using the expression system
CC can also be used to enhance TL5 activity. Diseases or susceptibility to a
CC disease can be diagnosed by determining the presence or absence of a
CC mutation in the TL5 protein. TL5 polynucleotides are useful for locating
CC genes associated with disease by hybridisation to chromosomes. TL5
CC polypeptides and polynucleotides can be used, especially to raise an
CC immune response (i.e. as vaccines) for the treatment of chronic and acute
CC inflammation, arthritis, septicemia, autoimmune diseases (e.g.
CC inflammatory bowel disease, psoriasis), transplant rejection,
CC graft vs. host disease, infection, stroke, ischaemia, acute respiratory
CC disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer
CC (e.g. lymphoproliferative disorders), atherosclerosis, and Alzheimers
CC disease.
XX
XX Sequence 285 AA;
XX
Query Match 100.0%; Score 1451; DB 19; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.4e-145;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDDSTEREQSLTSLCKKREMKKECVSILPRKESPSVRSGDKGLAATLLALLSCC 60
Db 1 MDDSTEREQSLTSLCKKREMKKECVSILPRKESPSVRSGDKGLAATLLALLSCC 60

QY 61 LTWVSFYQVAALQGLDLSRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFPEPPAP 120
Db 61 LTWVSFYQVAALQGLDLSRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFPEPPAP 120

QY 121 GEGNSSQNSRNKRAVQGPETVTQDCQLIADSEPTTIQKGSYTFVPWLLSFKRGSALEE 180
Db 121 GEGNSSQNSRNKRAVQGPETVTQDCQLIADSEPTTIQKGSYTFVPWLLSFKRGSALEE 180

QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQKRVHVFGEDELSTLFRCIQNMPETL 240
Db 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQKRVHVFGEDELSTLFRCIQNMPETL 240

QY 241 PNNSCYSAGIAKLEEGDELOLAIPRENAQISLDGVDVTFFGALKLL 285
Db 241 PNNSCYSAGIAKLEEGDELOLAIPRENAQISLDGVDVTFFGALKLL 285

RESULT 2
AAW62461
ID AAW62461 standard; Protein; 285 AA.
XX
AC AAW62461;
XX
XX 05-OCT-1998 (first entry)
XX
XX Human T cell surface antigen 63954 protein sequence #2.
XX
XX Human; 63954; primate; rodent; mouse; T cell surface antigen; mammal;
XX diagnosis; antigen-specific proliferation; cytokine production;
XX immune response; autoimmune disorder; rheumatoid arthritis;
XX systemic lupus erythematosus; Hashimoto's autoimmune thyroiditis.
XX
XX Homo sapiens.
XX
XX W09827114-A2.
XX

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PD 25-JUN-1998.
XX
PF 16-DEC-1997; 97WO-US23321.
XX
PR 17-DEC-1996; 96US-0033601.
XX
PA (SCHE ) SCHERING CORP.
XX
XX Gorman DM;
PI
DR WPI; 1998-362719/31.
DR N-PSDB; AAV39985.
XX
PT New isolated polypeptide, 63954 - used to develop products for
PT treating e.g. autoimmune disorders, inflammation, tissue rejection,
PT cancer or degenerative conditions
XX
XX Claim 1; Page 60-61; 69pp; English.
XX
XX The present sequence is a human T cell surface antigen, designated
XX 63954. The novel protein designated 63954 is expressed on T cells.
XX Protein 63954 can modulate antigen-specific proliferation and cytokine
XX production on effector cells and may potentiate immune cell expansion or
XX apoptosis. 63954 agonists or antagonists may also act as a co-stimulatory
XX molecule for regulation of T cell mediated cell activation, and may cause
XX a shift of T helper cell types, e.g. between Th1 and Th2. Antagonists of
XX 63954 can be used to modulate immune responses in abnormal situations,
XX e.g. autoimmune disorders, including rheumatoid arthritis, systemic
XX lupus erythematosus (SLE), Hashimoto's autoimmune thyroiditis, as well
XX as acute and chronic inflammatory responses in which T cell activation,
XX expansion, and/or immunological T cell memory play an important role,
XX such as chronic inflammation or tissue rejection. The products can also
XX be used in the treatment of conditions associated with abnormal
XX physiology or development, including abnormal proliferation, e.g.
XX cancerous conditions, or degenerative conditions. The products can also
XX be used for detection, diagnosis and drug screening.
XX
XX Sequence 285 AA;
XX
Query Match 100.0%; Score 1451; DB 19; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.4e-145;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDDSTEREQSLTSLCKKREMKKECVSILPRKESPSVRSGDKGLAATLLALLSCC 60
Db 1 MDDSTEREQSLTSLCKKREMKKECVSILPRKESPSVRSGDKGLAATLLALLSCC 60

QY 61 LTWVSFYQVAALQGLDLSRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFPEPPAP 120
Db 61 LTWVSFYQVAALQGLDLSRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFPEPPAP 120

QY 121 GEGNSSQNSRNKRAVQGPETVTQDCQLIADSEPTTIQKGSYTFVPWLLSFKRGSALEE 180
Db 121 GEGNSSQNSRNKRAVQGPETVTQDCQLIADSEPTTIQKGSYTFVPWLLSFKRGSALEE 180

QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQKRVHVFGEDELSTLFRCIQNMPETL 240
Db 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQKRVHVFGEDELSTLFRCIQNMPETL 240

QY 241 PNNSCYSAGIAKLEEGDELOLAIPRENAQISLDGVDVTFFGALKLL 285
Db 241 PNNSCYSAGIAKLEEGDELOLAIPRENAQISLDGVDVTFFGALKLL 285

RESULT 3
AAW58391
ID AAW58391 standard; Protein; 285 AA.
XX
AC AAW58391;
XX
XX 11-SEP-1998 (first entry)
XX
XX Homo sapiens neutrokin alpha protein.
XX

```


neutrokin alpha; cell proliferation; differentiation; migration; cytotoxicity; cell death; treatment; tumour; infection; inflammation; wound healing; immunodeficiency; autoimmune disease; graft rejection; fibrotic disorder; haematopoiesis; sepsis; shock; malaria; HIV; AIDS; acquired immune deficiency syndrome; rheumatoid arthritis; silicosis; cachexia; detection; diagnosis; drug screening.

Homo sapiens.

Key Domain Location/Qualifiers
 1..46 /note= "intracellular domain"
 47..72 /note= "transmembrane domain"
 73..285 /note= "extracellular domain"

WO9818921-A1.
 07-MAY-1998.
 25-OCT-1996; 96WO-US17957.
 25-OCT-1996; 96WO-US17957.
 (HUMA-) HUMAN GENOME SCI INC.

Ebner R, Ni J, Yu G;
 WPI; 1998-272216/24.
 N-PSDB; AAV30934.

New isolated human Neutrokin alpha - used to develop products for diagnosis and treatment of e.g. tumours, infections, immunodeficiencies or autoimmune diseases

Claim 17; Fig 1; 104pp; English.

The sequence is that of the neutrokin alpha protein.

Neutrokin alpha (NA) polypeptides modulate cell proliferation, differentiation, migration, cytotoxicity and cell death. They can be used to treat e.g. tumour and tumour metastasis, infections by bacteria, viruses and other parasites, immunodeficiencies, inflammatory diseases, lymphadenopathy, autoimmune diseases, graft versus host disease and to stimulate peripheral tolerance, destroy some transformed cell lines, mediate cell activation and proliferation, and are functionally linked as primary mediators of immune regulation, and inflammatory responses. Such activity is useful for immune enhancement or suppression, myeloprotection, stem cell mobilisation, acute and chronic inflammatory control and treatment of leukaemia. They can also be used to stimulate wound healing and to treat fibrotic disorders including liver cirrhosis, osteoarthritis and pulmonary fibrosis. They can also be used to regulate haematopoiesis, by regulating the activation and differentiation of various haematopoietic progenitor cells, e.g. to release mature leukocytes from the bone marrow following chemotherapy, and in stem cell mobilisation. NA may also be used to treat sepsis. NA antagonists can be used to prevent septic shock, inflammation, cerebral malaria, activation of the HIV virus, graft-host rejection, bone resorption, rheumatoid arthritis and cachexia (wasting or malnutrition). They can also be used to treat e.g. autoimmune diseases such as multiple sclerosis and insulin-dependent diabetes and inflammatory and infectious diseases such as silicosis, and sarcoidosis, idiopathic pulmonary fibrosis, idiopathic hyper-eosinophilic syndrome, endotoxic shock, atherosclerosis, histamine-mediated allergic reactions and immunological disorders including late phase allergic reactions, chronic urticaria, and atopic dermatitis by inhibiting chemokine-induced mast cell and basophil degranulation and release of histamine. IGE-mediated allergic reactions such as allergic asthma, rhinitis and eczema, inflammatory pulmonary diseases, rheumatoid arthritis, inflammation, degenerative and inflammatory arthropathies, aplastic anaemia, myelodysplastic syndrome, subepithelial basement membrane fibrosis or adult respiratory distress syndrome. The products can also be used for detection, diagnosis and

CC drug screening.
 XX
 SQ Sequence 285 AA;
 Query Match 100.0%; Score 1451; DB 19; Length 285;
 Best Local Similarity 100.0%; Pred. No. 4.4e-145;
 Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDDSTEREQSLTSCLLKREEMKLEKCVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
 |||||
 DB 1 MDDSTEREQSLTSCLLKREEMKLEKCVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
 |||||

QY 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKTFEPPAP 120
 |||||
 DB 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKTFEPPAP 120
 |||||

QY 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAALEE 180
 |||||
 DB 121 GEGNSSQNSRNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAALEE 180
 |||||

QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHILQKRVHVFGEDELSVTLFRCIONMPETL 240
 |||||
 DB 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHILQKRVHVFGEDELSVTLFRCIONMPETL 240
 |||||

QY 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDTFFFGALKLL 285
 |||||
 DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDTFFFGALKLL 285
 |||||

RESULT 4
 AAY22221
 ID AAY22221 standard; Protein; 285 AA.
 XX AC AAY22221;
 XX DT 16-SEP-1999 (first entry)
 XX DE Human TNF11 protein sequence.

XX TNF11; human; TNFR superfamily; tumour necrosis factor ligand; TNF;
 KW tumour necrosis factor receptor; TNFR superfamily; cell proliferation;
 KW cell differentiation; cytokine production; immunoglobulin; hyperplasia;
 KW apoptosis inducer; activated T cell; autoimmune disease; inhibitor;
 KW myasthenia gravis; insulin-dependent diabetes mellitus; endotoxic shock;
 KW rheumatoid arthritis; multiple sclerosis; systemic lupus erythematosus;
 KW tumour; proliferative disorder; neoplasia; dysplasia; immunocompetence;
 KW lymphoid organogenesis; bacterial resistance; contact hypersensitivity;
 KW delayed type sensitivity; therapy.

OS Homo sapiens.
 XX
 PN WO9933980-A2.
 XX
 PD 08-JUL-1999.
 XX
 PF 22-DEC-1998; 98WO-US27474.
 XX
 PR 16-DEC-1998; 98US-0212270.
 XX
 PR 30-DEC-1997; 97US-0068959.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Kassam A, Lamson G, Pot D, Tribouley C;
 XX
 DR WPI; 1999-405508/34.
 XX
 DR N-PSDB; AAX84620.
 XX
 PT New tumour necrosis factor ligands, useful for induction of cell death and/or proliferation of cells
 XX
 PS Claim 1; Page 61; 69pp; English.
 XX
 CC This sequence is the tumour necrosis factor (TNF) ligand family

CC protein of the invention, designated TNF1. The TNFL proteins play
 CC regulatory roles in cell proliferation and/or differentiation, e.g. they
 CC can induce production of cytokines, immunoglobulins, etc. A variety of
 CC diseases can be treated by modulating the activity of TNFL proteins,
 CC e.g. they can induce apoptosis of activated T cells but rescue resting
 CC T cell from apoptosis. TNFL polypeptides can therefore be used to treat
 CC autoimmune diseases, such as myasthenia gravis, insulin-dependent
 CC diabetes mellitus, rheumatoid arthritis, multiple sclerosis, and systemic
 CC lupus erythematosus. TNFL proteins also have tumour stimulating
 CC properties, so tumours can be treated by inhibiting the expression or
 CC activity of TNFL. Other proliferative disorders, such as neoplasias,
 CC dysplasias, and hyperplasia can also be treated using TNFL inhibitors.
 CC The TNFL polypeptides and polynucleotides can also be used to enhance or
 CC decrease TNF activity, thus providing therapeutic benefits such as
 CC induction of cell death, lymphoid organogenesis, or host bacterial
 CC resistance, and inhibition of endotoxic shock, contact hypersensitivity,
 CC delayed type sensitivity or immunocompetence of a transplant recipient.
 CC Tumour necrosis factor (TNF) and its receptors play a major role in host
 CC defence and immunosurveillance. As such, there is a need to identify new
 CC members of TNFR families. This invention provides this need.

XX Sequence 285 AA;

Query Match 100.0%; Score 1451; DB 20; Length 285;

Best Local Similarity 100.0%; Pred. No. 4.4e-145;

Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60
 |||||
 DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60
 |||||
 QY 61 LTVVSFYVAALQGDLSLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
 |||||
 DB 61 LTVVSFYVAALQGDLSLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
 |||||
 QY 121 GEGNSSQNRKRAVQGPETVTQDCLQLIADSETPTIQKGYTFVPWLLSFRKGSALAE 180
 |||||
 DB 121 GEGNSSQNRKRAVQGPETVTQDCLQLIADSETPTIQKGYTFVPWLLSFRKGSALAE 180
 |||||
 QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLLIQRKVHVFGDELSTLTLFRCIONMPETL 240
 |||||
 DB 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLLIQRKVHVFGDELSTLTLFRCIONMPETL 240
 |||||
 QY 241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGVTFFGALKLL 285
 |||||
 DB 241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGVTFFGALKLL 285
 |||||

RESULT 5

AA04392

ID AAY04392 standard; Protein; 285 AA.

XX

AC AAY04392;

XX

DT 24-JUN-1999 (first entry)

XX

DE Human Kay-ligand.

XX

XX Kay-ligand; tumour necrosis factor family; TNF; Immune system;
 KW cytokine; autoimmune disease; tissue graft; cancer; cell death.

XX

OS Homo sapiens.

XX

PN WO9912964-A2.

XX

PD 18-MAR-1999.

XX

PF 11-SEP-1998; 98WO-US19037.

XX

PR 12-SEP-1997; 97US-0058786.

XX

XX (BIOJ) BIOGEN INC.

PA

PI Tschopp J;

XX

DR WPI: 1999-243715/20.

DR

DR N-PSDB; AAX33330.

XX

PT New human or murine Kay-ligands, members of the tumour necrosis

XX

PS Claim 12; Page 32; 41pp; English.

XX

CC The present sequence represents human Kay-ligand, which is a member of
 CC the tumour necrosis factor (TNF) family of cytokines. Pharmaceutical
 CC compositions containing the Kay-ligand can be used to suppress or
 CC stimulate the immune system, especially to prevent or reduce the
 CC severity of autoimmune diseases or response to a tissue graft or to
 CC treat cancer. An agent capable of interfering with the Kay-ligand can be
 CC used to induce cell death. The Kay-ligand can also be used to identify
 CC its receptors.

XX Sequence 285 AA;

Query Match 100.0%; Score 1451; DB 20; Length 285;

Best Local Similarity 100.0%; Pred. No. 4.4e-145;

Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60
 |||||
 DB 1 MDDSTEREQSLTSCCLKREEMKKECVSILPRKESPSVRSKDGKLLAATLLALLSCC 60
 |||||
 QY 61 LTVVSFYVAALQGDLSLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
 |||||
 DB 61 LTVVSFYVAALQGDLSLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
 |||||
 QY 121 GEGNSSQNRKRAVQGPETVTQDCLQLIADSETPTIQKGYTFVPWLLSFRKGSALAE 180
 |||||
 DB 121 GEGNSSQNRKRAVQGPETVTQDCLQLIADSETPTIQKGYTFVPWLLSFRKGSALAE 180
 |||||
 QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLLIQRKVHVFGDELSTLTLFRCIONMPETL 240
 |||||
 DB 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLLIQRKVHVFGDELSTLTLFRCIONMPETL 240
 |||||
 QY 241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGVTFFGALKLL 285
 |||||
 DB 241 PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGVTFFGALKLL 285
 |||||

RESULT 6

AAW93586

ID AAW93586 standard; Protein; 285 AA.

XX

AC AAW93586;

XX

DT 18-JUN-1999 (first entry)

XX

DE Human TNRL1-alpha protein.

XX

Tumour necrosis factor receptor; signal transducer molecule; TNF; APO4;
 KW developmental abnormality; gestational abnormality; prostate cancer;
 KW APO6; APO8; APO9; TNRL-1; TNRL-3; diagnosis; treatment; therapy; disease;
 KW cytoplasmic domain; immunogen; antibody preparation; breast carcinoma;
 KW apoptosis; human; TNRL1-alpha.

XX

OS Homo sapiens.

XX

PN WO9911791-A2.

XX

PD 11-MAR-1999.

XX

PF 04-SEP-1998; 98WO-US18393.

XX

PR 05-SEP-1997; 97US-0924634.

XX

XX (UNIW) UNIV WASHINGTON.

PA

XX Chaudhary PM;
 XX WPI; 1999-205191/17.
 XX N-PSDB; AAX23420.
 XX New Tumor Necrosis Factor family receptor polypeptides and ligands -
 XX useful for diagnosis and treatment of prostate cancer and
 XX developmental or gestational abnormalities
 XX Claim 34; Fig 11A; 156pp; English.
 XX This invention describes isolated Tumor Necrosis Factor (TNF) family
 XX receptor polypeptides; APO4, APO6, APO8 and APO9 or their active
 XX fragments, and isolated TNF related ligands 1 and 3 (TNRL1 and TNRL3) or
 XX their active fragments. APO4 is useful for diagnosing prostate cancer
 XX by determining levels of APO4 in an individual. Prostate cancer can also
 XX be treated using APO4 selective binding agents linked to a therapeutic
 XX moiety. APO4 polypeptides are also useful for identifying selective
 XX binding agents, useful in diagnosis/treatment of disease by binding of
 XX agents to the polypeptide/active fragment which is extracellular, or
 XX expressed on the cell surface. The binding is preferably performed in
 XX vivo. APO4 polypeptides/active fragments are also useful for screening
 XX for agonists and antagonists by binding and observing the change in APO4
 XX activity. Effective pharmacological agents useful in diagnosis or
 XX treatment of disease are also identified using APO4 polypeptides/active
 XX fragments and APO4 signal transducer molecules that specifically interact
 XX with a cytoplasmic domain of APO4 and detecting a change in level of APO4
 XX activity. The method is performed in vivo or in vitro. APO polypeptides
 XX are all useful as immunogens for preparing antibodies. APO4 is also
 XX useful for diagnosis/treatment of developmental or gestational
 XX abnormalities. APO8 was transfected to human breast carcinoma cell line
 XX MCF-7, and induced apoptosis.
 XX Sequence 285 AA;
 XX
 Query Match 100.0%; Score 1451; DB 20; Length 285;
 Best Local Similarity 100.0%; Pred. No. 4.4e-145;
 Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDDSTERQSLTSCILKREEMKKECVSILPRKESPSVRSSKDKGLLAATLLALLSCC 60
 DB 1 MDDSTERQSLTSCILKREEMKKECVSILPRKESPSVRSSKDKGLLAATLLALLSCC 60
 QY 61 LTVVSFYQVAALQGLDASLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
 DB 61 LTVVSFYQVAALQGLDASLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
 QY 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVFWLLSFKRGSALRE 180
 DB 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVFWLLSFKRGSALRE 180
 QY 181 KENKILVKETGYFFIYGVLYTDKTYAMGHLIQRKVVHVFQDGLSLVTLFRQIONMPETL 240
 DB 181 KENKILVKETGYFFIYGVLYTDKTYAMGHLIQRKVVHVFQDGLSLVTLFRQIONMPETL 240
 QY 241 PNNSCYSAGTAKLEEGDELQALPRENAQISLDGVDVTFEGALKLL 285
 DB 241 PNNSCYSAGTAKLEEGDELQALPRENAQISLDGVDVTFEGALKLL 285
 RESULT 7
 AAB28553
 ID AAB28553 standard; protein; 285 AA.
 XX
 AC AAB28553;
 XX
 DT 08-FEB-2001 (first entry)
 XX
 XX Human TNFL1.
 DE
 XX Human; tumour necrosis factor like-1; TNFL1; tumour necrosis factor; TNF;
 KW immunosuppressive; antiarthritic; neuroprotective; dermatological;

KW antinflammatory; antidiabetic; cytostatic; osteopathic; gene therapy;
 KW colon cancer; rheumatoid arthritis; septic shock; Crohn's disease;
 KW osteoporosis; autoimmune disease; myasthenia gravis;
 KW insulin-dependent diabetes mellitus.
 OS Homo sapiens.
 XX
 XX WO200060079-A2.
 PN
 XX 12-OCT-2000.
 PD
 XX 05-APR-2000; 2000WO-US09058.
 PF
 XX 05-APR-1999; 99US-0286529.
 PR
 XX (CHIR) CHIRON CORP.
 PA
 XX Tribouley C;
 PI
 XX WPI; 2000-665004/64.
 DR N-PSDB; AAC63756.
 XX
 XX Tumor necrosis factor (TNF) and TNF receptor superfamily protein
 XX members TNF-L and TNFR-L, useful for enhancing or decreasing TNF
 XX activities such as inducing cell death and lymphoid organogenesis
 XX
 PS Claim 1; Page 65; 77pp; English.
 XX
 CC The present sequence is given in a specification relating to an isolated
 CC human protein designated tumour necrosis factor like-1 (TNFL1). It may be
 CC used to induce cell death in tumours, to induce apoptosis of activated T
 CC cells, to induce inflammation, and to rescue resting T cells from
 CC apoptosis. TNF receptors are used to regulate the function of a TNF
 CC ligand which plays a role in apoptosis, inflammation, differentiation, or
 CC proliferation. Expression of the receptors can also be useful as markers
 CC for cancer, especially for colon cancer. Diseases which can be treated
 CC using ligands and/or receptors of the TNF/TNFR superfamily include
 CC rheumatoid arthritis, cancer, septic shock, Crohn's disease and
 CC osteoporosis. The polynucleotides can be used in gene delivery vehicles,
 CC for the purpose of delivering a mRNA or oligonucleotide, full-length
 CC protein, fusion protein, polypeptide, or ribozyme, or single-chain
 CC antibody, into a cell. The newly identified receptor proteins play
 CC regulatory roles in cell proliferation and/or differentiation. The
 CC receptors can also play a role in the negative regulation of
 CC osteoclastogenesis. Soluble TNFR-like receptors can be useful in the
 CC neutralisation of TNF or TNF-like ligands. A TNF-L protein can also be
 CC used to treat autoimmune diseases (myasthenia gravis and
 CC insulin-dependent diabetes mellitus), tumours, and proliferative
 CC disorders. A TNF-L or TNFR-L subgenomic polynucleotide can also be
 CC delivered to subjects for the purpose of screening test compounds for
 CC those which are useful for enhancing transfer of TNF-L subgenomic
 CC polynucleotides to the cell or for enhancing subsequent biological
 CC effects of TNF-L or TNFR-L subgenomic polynucleotides within the cell.
 XX
 XX Sequence 285 AA;
 Query Match 100.0%; Score 1451; DB 21; Length 285;
 Best Local Similarity 100.0%; Pred. No. 4.4e-145;
 Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MDDSTERQSLTSCILKREEMKKECVSILPRKESPSVRSSKDKGLLAATLLALLSCC 60
 DB 1 MDDSTERQSLTSCILKREEMKKECVSILPRKESPSVRSSKDKGLLAATLLALLSCC 60
 QY 61 LTVVSFYQVAALQGLDASLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
 DB 61 LTVVSFYQVAALQGLDASLRAELQGHHAELKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
 QY 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVFWLLSFKRGSALRE 180
 DB 121 GEGNSSQNRKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVFWLLSFKRGSALRE 180
 QY 181 KENKILVKETGYFFIYGVLYTDKTYAMGHLIQRKVVHVFQDGLSLVTLFRQIONMPETL 240

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Db 181 KENKILVKEGYFFIYGVLYTDKTYAMGHLQKRVHVGDELSLVTLFRCIQNMPETL 240
QY 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285
Db 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285

RESULT 8
AAB08659
ID AAB08659 standard; Protein; 285 AA.
AC AAB08659;
XX
DT 02-JAN-2001 (first entry)
XX
DE Amino acid sequence of a human neutrokinine-alpha polypeptide.
XX
KW Human; neutrokinine-alpha; tumor; tumor metastasis; infection;
KW immunodeficiency; inflammatory disease; lymphadenopathy; dermatitis;
KW autoimmune disease; graft versus host disease; immune regulation;
KW severe combined immunodeficiency-X-linked agammaglobulinemia;
KW kappa chain deficiency; B cell lymphoproliferative disorder; purpura;
KW Wiskott-Aldrich syndrome; systemic lupus erythematosus; myocarditis;
KW idiopathic thrombocytopenia purpura; hemolytic anemia; neuritis;
KW allergic encephalomyelitis; relapsing polychondritis; glomerulonephritis;
KW rheumatic heart disease; multiple sclerosis; uveitis; ophthalmia;
KW polyendocrinopathy; Reiter's disease; autoimmune pulmonary inflammation;
KW myeloprotection; stem cell mobilization; leukemia.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Domain 1..46
FT /note= "intracellular domain"
FT Domain 47..72
FT /note= "transmembrane domain"
FT Domain 73..285
FT /note= "extracellular domain"
FT Modified-site 124..127
FT /note= "potential N-linked glycosylation site"
FT Modified-site 242..245
FT /note= "potential N-linked glycosylation site"
XX
PN WO200050597-A2.
XX
XX 31-AUG-2000.
XX
XX 22-FEB-2000; 2000WO-US04336.
XX
XX 23-FEB-1999; 99US-0255794.
XX 02-MAR-1999; 99US-0122388.
XX 12-MAR-1999; 99US-0124097.
XX 26-MAR-1999; 99US-0126599.
XX 02-APR-1999; 99US-0127598.
XX 16-APR-1999; 99US-0130412.
XX 23-APR-1999; 99US-0130696.
XX 27-APR-1999; 99US-0131278.
XX 29-APR-1999; 99US-0131673.
XX 28-MAY-1999; 99US-0136784.
XX 06-JUL-1999; 99US-0142659.
XX 27-JUL-1999; 99US-0145824.
XX 24-NOV-1999; 99US-0167239.
XX 03-DEC-1999; 99US-0168624.
XX 16-DEC-1999; 99US-0171108.
XX 23-DEC-1999; 99US-0171626.
XX 14-JAN-2000; 2000US-0176015.
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ni J, Ebner R, Yu G;
XX WPI; 2000-572093/53.
XX

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DR N-PSDB; AAA64427.
XX
PT Novel cytokine neutrokinine-alpha, its splicing variant, neutrokinine-alpha
PT SV polypeptides useful for treating tumor, tumor metastasis, microbial
PT infections, immunodeficiency, inflammatory diseases, lymphadenopathy
PT
XX
PS Claim 18; Fig 1A-B; 414pp; English.
XX
XX The present sequence represents a human neutrokinine-alpha polypeptide.
XX Neutrokinine-alpha polypeptides are used to treat, prevent, prognosis and
XX diagnose tumor and tumor metastasis, infections by bacteria, viruses
XX and other parasites, immunodeficiencies, inflammatory diseases,
XX lymphadenopathy, autoimmune diseases, graft versus host diseases, to
XX mediate immune regulation and inflammatory responses. Diseases which
XX may be treated include severe combined immunodeficiency (SCID)-X-linked
XX agammaglobulinemia, kappa chain deficiency, B cell lymphoproliferative
XX disorder (BLPD), Wiskott-Aldrich syndrome, systemic lupus erythematosus,
XX idiopathic thrombocytopenia purpura, hemolytic anemia, dermatitis,
XX allergic encephalomyelitis, myocarditis, relapsing polychondritis,
XX rheumatic heart disease, glomerulonephritis, multiple sclerosis,
XX neuritis, Uveitis Ophthalmia, Polyendocrinopathies, Purpura
XX (e.g. Henoch-Schoenlein purpura), Reiter's Disease, and Autoimmune
XX Pulmonary Inflammation. Neutrokinine-alpha is useful for immune
XX enhancement or suppression, myeloprotection, stem cell mobilization,
XX acute and chronic inflammatory control and treatment of leukemia.
XX
SQ Sequence 285 AA;
XX
Query Match 100.0%; Score 1451; DB 21; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.e-145;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDDSTEREQSLTSCIAKREMKKECVSTLPRKESPSVRSXGKLLAATLLALLSCC 60
DB 1 MDDSTEREQSLTSCIAKREMKKECVSTLPRKESPSVRSXGKLLAATLLALLSCC 60
QY 61 LTVVSFYQVAALQGLDASLRAELQGHHAELKAGAPKAGLEAPAVTAGLIFPPAP 120
DB 61 LTVVSFYQVAALQGLDASLRAELQGHHAELKAGAPKAGLEAPAVTAGLIFPPAP 120
QY 121 GEGNSSONSRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFRGSALEE 180
DB 121 GEGNSSONSRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFRGSALEE 180
QY 181 KENKILVKETGYFFIYGVLYTDKTYAMGHLQKRVHVGDELSLVTLFRCIQNMPETL 240
DB 181 KENKILVKETGYFFIYGVLYTDKTYAMGHLQKRVHVGDELSLVTLFRCIQNMPETL 240
QY 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285
DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGVDVTFFGALKLL 285

RESULT 9
AAB08191
ID AAB08191 standard; Protein; 285 AA.
XX
AC AAB08191;
XX
DT 04-DEC-2000 (first entry)
XX
DE Amino acid sequence of human cytokine designated THANK.
XX
KW Human; cytokine; THANK; tumour necrosis factor homologue; apoptosis;
KW nuclear factor-kB; c-jun N-terminal kinase; shock; acute phase response;
KW viral infection; radiation susceptibility; atherosclerosis; cancer;
KW acute inflammatory condition; arthritis; allergy;
KW graft versus host reaction; tumour cell.
XX
XX Homo sapiens.
XX
XX OS
XX Key Location/Qualifiers
FH

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FT Domain 1..46
FT /note= "intracellular domain"
FT 47..77
FT /note= "transmembrane domain"
FT 78..111
FT /note= "extracellular domain"
FT 112..285
FT /note= "extracellular domain"
XX
PN WO200045836-A1.
XX
XX 10-AUG-2000.
XX
XX 02-FEB-2000; 2000WO-US02751.
XX
XX 02-FEB-1999; 99US-0118531.
XX
PA (RERE-) RES DEV FOUND.
XX
XX Aggarwal BB;
XX
XX WPI; 2000-514890/46.
XX
XX Inhibiting the activation of nuclear factor-kB in cells for treating
XX pathological conditions comprises treating cells with a tumour necrosis
XX factor homolog inhibitor -
XX
XX Example 1; Fig 1; 45pp; English.
XX
XX The present sequence represents a human cytokine, designated THANK.
XX THANK is a tumour necrosis factor (TNF) homologue that activates
XX apoptosis, nuclear factor-kB, and c-Jun N-terminal kinase. Inhibitors of
XX the THANK polypeptide are used to inhibit the activation of nuclear
XX factor-kB in cells. The method is used to inhibit the activation of
XX nuclear factor-kB in cells, treat pathological conditions such as toxic
XX and septic shock, acute phase response, viral infection, radiation
XX susceptibility, atherosclerosis, cancer, acute inflammatory conditions,
XX arthritis, allergy, and graft versus host reaction, and inhibit growth
XX of tumour cells such as myeloid cells, colon cancer cells, prostate
XX cancer cells, cervical carcinoma cells, chronic myeloid leukemic cells
XX and acute myeloid leukemic cells.
XX
XX Sequence 285 AA;

Query Match 100.0%; Score 1451; DB 21; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.4e-145;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDDSTEREQSLTSCCLKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
Db 1 MDDSTEREQSLTSCCLKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60

QY 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
Db 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120

QY 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSAL 180
Db 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSAL 180

QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQKRVHVFGEDELSVTLFRCIQNMPETL 240
Db 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLIQKRVHVFGEDELSVTLFRCIQNMPETL 240

QY 241 PNNCSYAGIAKLEEGDELQIAIPRENAQISLDGVDVTFFGALKLL 285
Db 241 PNNCSYAGIAKLEEGDELQIAIPRENAQISLDGVDVTFFGALKLL 285

RESULT 10
AAB08261
ID AAB08261 standard; Protein; 285 AA.
XX

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AC AAB08261;
XX
XX 04-DEC-2000 (first entry)
XX
XX Amino acid sequence of a human AGP-3 polypeptide.
XX
XX AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
XX type II transmembrane protein; B cell stimulatory factor;
XX inflammatory disorder; immune disorder; rheumatoid arthritis;
XX lupus and graft versus host disease.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 1..46
XX /note= "intracellular domain"
XX Region 42..72
XX /note= "transmembrane region"
XX Domain 73..285
XX /note= "extracellular domain"
XX
XX WO200047740-A2.
XX
XX 17-AUG-2000.
XX
XX 11-FEB-2000; 2000WO-US03653.
XX
XX 12-FEB-1999; 99US-0119906.
XX 18-NOV-1999; 99US-0166271.
XX
XX (AMGE-) AMGEN INC.
XX
XX Boyle WJ, Hsu H;
XX WPI; 2000-558217/51.
XX N-PSDB; AAA63941.
XX
XX Novel polypeptides comprising tumour necrosis factor ligand family
XX proteins, useful for treating inflammatory and immune disorders, e.g.
XX rheumatoid arthritis -
XX
XX Claim 4; Fig 1; 71pp; English.
XX
XX The present sequence represents a human AGP-3 polypeptide. AGP-3 is a
XX tumour necrosis factor (TNF) ligand family member. AGP-3 is a type II
XX transmembrane protein, and is a potent B cell stimulatory factor.
XX Expression of AGP-3 correlates to increases in the number of B cells
XX and immunoglobulins produced. AGP-3 proteins, antibodies, and nucleic
XX acids may be used to treat inflammatory and immune disorders,
XX e.g. rheumatoid arthritis, Crohn's disease, lupus and graft versus
XX host disease. The nucleic acids may be used to regulate the expression
XX of an AGP-3 related protein. The AGP-3 proteins, antibodies and nucleic
XX acids are also useful for the detection of AGP-3 agonists, antagonists
XX and characterizing interactions with AGP-3 related proteins.
XX note: this sequence is not specifically claimed. It is only mentioned
XX in the claims, in that a polypeptide that does not comprise the present
XX sequence is claimed.
XX
XX Sequence 285 AA;

Query Match 100.0%; Score 1451; DB 21; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.4e-145;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDDSTEREQSLTSCCLKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
Db 1 MDDSTEREQSLTSCCLKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60

QY 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
Db 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120

QY 121 GEGNSSQNSRNKRAVQGPETVTQDCLQIADSETPTIQKGSYTFVPWLLSFKRGSAL 180

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Db 121 GEGNSSQNRKRAVQGPETVTQDCQLIADSETPTIQKGSYTFVPWLLSFKRGSALAE 180
Qy 181 KENKILVKETGYFFIYGQVLYTKTYAMGHLIQRKKVHVFGDELSLVTFRICQNMPETL 240
Db 181 KENKILVKETGYFFIYGQVLYTKTYAMGHLIQRKKVHVFGDELSLVTFRICQNMPETL 240
Qy 241 PNNCSYSAGIAKLEEGDELQLAIPRENAQISLDGDTFFGALKLL 285
Db 241 PNNCSYSAGIAKLEEGDELQLAIPRENAQISLDGDTFFGALKLL 285

RESULT 11
AAE09242
ID AAE09242 standard; Protein; 285 AA.
XX AC AAE09242;
XX DT 19-NOV-2001 (first entry)
XX DE Human TALL-1 protein.
XX KW Human; TNF; tumour necrosis factor; TALL-1; APRIL; TNF receptor;
KW TNFR; TACI; BCMA; therapy; cancer; leukaemia; myeloma; lymphoma;
KW autoimmune disease; rheumatoid arthritis; multiple sclerosis;
KW psoriasis.
XX OS Homo sapiens.
XX PN W0200160397-A1.
XX PD 23-AUG-2001.
XX PF 28-NOV-2000; 2000WO-US32378.
XX PR 16-FEB-2000; 2000US-0182938.
XX PR 22-AUG-2000; 2000US-0226986.
XX PA (GETH ) GENENTECH INC.
XX PI Ashkenazi AJ, Dodge KH, Grewal I, Kim KJ, Marsters SA, Pitti RM;
XX PI Yan M;
XX WPI: 2001-541628/60.
XX N-PSDB; AAD15903.
XX PT Inhibiting or neutralizing TALL-1 or APRIL polypeptide biological
XX PT activity, for treating autoimmune disorders and cancer, comprises
XX PT exposing the cells to TALL-1 or APRIL polypeptide agonists or
XX PT antagonists.
XX PS Claim 2; Fig 3; 160pp; English.
XX CC The invention relates to methods of using one or more agonists or
XX CC antagonists to modulate the activity of the members of TNF (tumour
XX CC necrosis factor) especially TALL-1, APRIL and TNF receptor (TNFR)
XX CC e.g. TACI or BCMA. The method is useful for treating pathological
XX CC conditions or diseases associated with increased TALL-1 and APRIL
XX CC expression or activity. TALL-1 and APRIL antagonists are used to
XX CC block the interaction between APRIL and TALL-1 with TACI or BCMA.
XX CC They are useful for treating a mammal suffering from cancer such
XX CC as leukaemia, lymphoma, myeloma, cancers of lung and colon and
XX CC autoimmune diseases e.g. rheumatoid arthritis, multiple sclerosis,
XX CC psoriasis and lupus erythematosus. The present sequence is human
XX CC TALL-1 protein.
XX SQ Sequence 285 AA;

Query Match 100.0%; Score 1451; DB 22; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.4e-145;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDDSTEREQSLTCLKKREMKKECVSILPRKESVSRSSKDGKLLAATLLALLSCC 60

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Db 1 MDDSTEREQSLTCLKKREMKKECVSILPRKESVSRSSKDGKLLAATLLALLSCC 60
Qy 61 LTVVSFYQVAALQDGLASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKTFEPAP 120
Db 61 LTVVSFYQVAALQDGLASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKTFEPAP 120
Qy 121 GEGNSSQNRKRAVQGPETVTQDCQLIADSETPTIQKGSYTFVPWLLSFKRGSALAE 180
Db 121 GEGNSSQNRKRAVQGPETVTQDCQLIADSETPTIQKGSYTFVPWLLSFKRGSALAE 180
Qy 181 KENKILVKETGYFFIYGQVLYTKTYAMGHLIQRKKVHVFGDELSLVTFRICQNMPETL 240
Db 181 KENKILVKETGYFFIYGQVLYTKTYAMGHLIQRKKVHVFGDELSLVTFRICQNMPETL 240
Qy 241 PNNCSYSAGIAKLEEGDELQLAIPRENAQISLDGDTFFGALKLL 285
Db 241 PNNCSYSAGIAKLEEGDELQLAIPRENAQISLDGDTFFGALKLL 285

RESULT 12
AAE07156
ID AAE07156 standard; Protein; 285 AA.
XX AC AAE07156;
XX DT 06-NOV-2001 (first entry)
XX DE Human tumour necrosis factor (TNF)-delta protein.
XX KW Human; tumour necrosis factor; TNF-delta; gene therapy; antirheumatic;
KW apoptosis; rheumatoid arthritis; cytostatic; sepsis; anti-inflammatory;
KW inflammatory bowel disease; immunosuppressive; antiarthritic; tumour;
KW antibacterial; cancer.
XX OS Homo sapiens.
XX PN US2001010925-A1.
XX PD 02-AUG-2001.
XX PF 17-NOV-1997; 97US-0971317.
XX PR 17-NOV-1997; 97US-0971317.
XX PA (WILEY) WILEY S R.
XX PI Wiley SR;
XX WPI: 2001-496166/54.
XX N-PSDB; AAD13435.
XX PT New tumor necrosis factors (TNF)-delta polynucleotide and polypeptide,
XX PT useful in gene therapy, particularly for treating inflammation, and for
XX PT inducing apoptosis in cancer and tumor-associated cells to treat cancer
XX PS Claim 16; Page 36-37; 46pp; English.
XX CC The present sequence is human tumor necrosis factor (TNF)-delta protein.
XX CC The TNF-delta polynucleotide is useful in gene therapy for modulating
XX CC TNF-delta. TNF-delta is useful for treating deficiencies of TNF-delta
XX CC and diseases ameliorated by TNF-delta. TNF-delta is also useful for
XX CC screening, diagnosing, prognosing, staging or monitoring conditions
XX CC or diseases attributable to TNF-delta, e.g. inflammation (e.g.
XX CC inflammatory bowel disease, sepsis or rheumatoid arthritis). The
XX CC TNF-delta is also useful as an anti-cancer agent to induce apoptosis in
XX CC cancer and tumour-associated cells.
XX SQ Sequence 285 AA;

Query Match 100.0%; Score 1451; DB 22; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.4e-145;

```

Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDDSTEREQSLTCLKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
 DB 1 MDDSTEREQSLTCLKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
 QY 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
 DB 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
 QY 121 GEGNSSONSNNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL 180
 DB 121 GEGNSSONSNNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL 180
 QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLLQKRVHVGDELSLVTFLFRQIONMPETL 240
 DB 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLLQKRVHVGDELSLVTFLFRQIONMPETL 240
 QY 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDTFFGALKLL 285
 DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDTFFGALKLL 285

RESULT 13
 AA07879 AAE07879 standard; Protein; 285 AA.
 XX
 AC AAE07879;
 XX
 DT 01-NOV-2001 (first entry)
 XX
 DE Human BAFF protein.
 XX
 KW Human; tumour necrosis factor; TNF; APBF; APRIL; BAFF; therapy; melanoma;
 KW immune system-related disorder; cancer; renal cell; breast; stomach;
 KW rectal; colon; throat; bladder; ovarian carcinoma; cellular disorder;
 KW gastrointestinal; scleroderma; Kaposi's sarcoma; chronic leukaemia;
 KW squamous cell carcinoma; hyperproliferative condition; pannus formation;
 KW rheumatoid arthritis; postsurgical scarring; fibrosis; liver; uterine;
 KW lung; immunodeficiency; inflammatory disease; lymphadenopathy; vulnary;
 KW autoimmune disease; graft versus host disease; dermatological;
 KW antiinflammatory; immunosuppressive; cytostatic.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..46
 FT /label= Intracellular_domain
 FT Domain 47..72
 FT /label= Transmembrane_domain
 FT Domain 73..285
 FT /label= Extracellular_domain
 XX
 FN WO200158949-A2.
 XX
 PD 16-AUG-2001.
 XX
 PE 08-FEB-2001; 2001WO-US04121.
 XX
 PR 11-FEB-2000; 2000US-0181670.
 XX
 PA (BIOJ) BIOGEN INC.
 XX
 PI Rennert PD, Thompson JS, Ambrose C, Cachero TG;
 XX
 DR WPI; 2001-514644/56.
 DR N-PSDB; AAD14417.
 XX
 PT New heteromeric ligand of tumor necrosis factor (TNF) family, useful
 PT for diagnosis, treatment of immune system-related disorders in humans,
 PT comprises TNF-family member APRIL subunit linked non-covalently to
 PT TNF-family member BAFF subunit -
 XX

PS Claim 2; Fig 2b; 42pp; English.
 XX
 CC The present invention relates to an isolated heteromeric ligand of
 CC tumour necrosis factor (TNF)-family, referred to as APBF comprising a
 CC TNF-family member APRIL subunit linked non-covalently to TNF-family
 CC member BAFF subunit. APBF is useful for diagnosis or treatment of
 CC various immune system-related disorders in mammals, preferably humans.
 CC Such disorders include cancer, including cellular disorders, for e.g.
 CC renal cell cancer, Kaposi's sarcoma, chronic leukaemia, breast cancer,
 CC sarcoma, ovarian carcinoma, rectal cancer, throat cancer, melanoma,
 CC colon cancer, bladder cancer, squamous cell carcinoma and
 CC gastrointestinal or stomach cancer, cellular hyperproliferative
 CC conditions, such as scleroderma, pannus formation in rheumatoid
 CC arthritis, postsurgical scarring and lung, liver and uterine fibrosis
 CC and immunodeficiencies, inflammatory diseases, lymphadenopathy,
 CC autoimmune diseases and graft versus host disease. APBF is also useful
 CC for producing monoclonal or polyclonal antibodies and for identifying
 CC novel modulators affecting biological function and for identifying
 CC with APBF. The present sequence is human BAFF protein.
 XX
 SQ Sequence 285 AA;

Query Match 100.0%; Score 1451; DB 22; Length 285;
 Best Local Similarity 100.0%; Pred. No. 4.4e-145;
 Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDDSTEREQSLTCLKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
 DB 1 MDDSTEREQSLTCLKKREEMKKECVSILPRKESPSVRSSKDGKLLAATLLALLSCC 60
 QY 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
 DB 61 LTVVSFYQVAALQGDLSLRAELQGHAEKLPAGAPKAGLEAPAVTAGLKIFEPAP 120
 QY 121 GEGNSSONSNNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL 180
 DB 121 GEGNSSONSNNKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSFKRGSAL 180
 QY 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLLQKRVHVGDELSLVTFLFRQIONMPETL 240
 DB 181 KENKILVKETGYFFIYGQVLYTDKTYAMGHLLQKRVHVGDELSLVTFLFRQIONMPETL 240
 QY 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDTFFGALKLL 285
 DB 241 PNNCSYAGIAKLEEGDELQLAIPRENAQISLDGDTFFGALKLL 285

RESULT 14
 AAU12183
 ID AAU12183 standard; Protein; 285 AA.
 XX
 AC AAU12183;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE Human PRO738 polypeptide sequence.
 XX
 KW Human secretory and transmembrane; PRO; mammalian; cancer; lung;
 KW breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;
 KW cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;
 KW adipocyte; A-peptide; factor VIIA; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO20010466-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 01-DEC-2000; 2000WO-US32678.
 XX
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.
PR 02-DEC-1999; 99WO-US28565.
PR 09-DEC-1999; 99US-0170262.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 20-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US31243.
PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US0376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 10-NOV-2000; 2000WO-US30873.
XX (GETH) GENENTECH INC.
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
PI Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WL, Zhang Z;
XX WPI; 2001-408281/43.
DR N-PSDB; AAS21255.
XX Isolated, secretory and transmembrane PRO polypeptide used to detect
PT other PRO polypeptides, link bioactive molecules to cells expressing
PT PRO polypeptides, and detect the presence of mammalian tumours e.g.
XX lung, breast, prostate, cervical
XX Claim 12; Fig 24; 813pp; English.
XX AAU12172-AAU12446 represent novel human secretory and transmembrane
CC PRO polypeptides. The PRO polypeptides are useful to detect other
CC PRO polypeptides, to link bioactive molecules to cells expressing
CC PRO polypeptides, to modulate biological activities of cells expressing
CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
CC polypeptide expression in a cell sample to that in a control sample.
CC Some of the 275 sequences are also useful to stimulate the release of
CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
CC proliferation or differentiation of chondrocytes, the proliferation or
CC gene expression in pericyte cells, the release of proteoglycans from
CC cartilage, the proliferation of inner ear utricular supporting cells or
CC of T-lymphocytes, the release of a cytokine from peripheral blood
CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
CC to factor VIIA. The PRO polypeptides can be used in assays to identify
CC molecules involved in binding interactions. The polynucleotides encoding
CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
CC transgenic or knock out animals and can be used in gene therapy.
XX Sequence 285 AA;
SQ Query Match 100.0%; Score 1451; DB 22; Length 285;
Best Local Similarity 100.0%; Pred. No. 4.4e-145;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDDSTERGSRUTCLCKKEEMKKECVSILPRKESPSVRSGDKGLAATLLALLSCC 60
DB 1 MDDSTERGSRUTCLCKKEEMKKECVSILPRKESPSVRSGDKGLAATLLALLSCC 60
QY 61 LTVVSFYQVAALQGLDASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120

Db 61 LTVVSFYQVAALQGLDASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
QY 121 GEGNSSQNRKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSPFRGSALEE 180
Db 121 GEGNSSQNRKRAVQGPETVTQDCLQLIADSETPTIQKGSYTFVPWLLSPFRGSALEE 180
QY 181 KENKILVKETGYFFIYGQVLYTKTYAMGHLIQKVKVHVFGEDELSTVTLFRCIQNMPETL 240
Db 181 KENKILVKETGYFFIYGQVLYTKTYAMGHLIQKVKVHVFGEDELSTVTLFRCIQNMPETL 240
QY 241 PNNCSYSGIAKLEEGDELQLAIPRENAQISLDGDTFFGALKLL 285
Db 241 PNNCSYSGIAKLEEGDELQLAIPRENAQISLDGDTFFGALKLL 285
RESULT 15
AAU12172
ID AAY71915 standard; Protein; 285 AA.
XX AAY71915;
AC AAY71915;
DT 26-MAR-2001 (first entry)
XX Human TACI-Ligand (TACI-L) protein.
XX Human; transmembrane activator and CAML interactor; TACI;
KW tumour necrosis factor receptor; TNF; autoimmune disease; diabetes;
KW calcium-signal modulating cyclophilin ligand; CAML; viral infection;
KW neutrophilic alpha polypeptide; TACI-Ligand; TACI-L; cytostatic; therapy;
KW neuroprotective; antidiabetic; antiviral; antiinflammatory; tumour;
KW antiarthritic; antirheumatic; immunosuppressive; multiple sclerosis;
KW rheumatoid arthritis; graft rejection; inflammation; cell proliferation;
KW cell death; immunoglobulin E-mediated allergic reaction; IgE.
XX Homo sapiens.
XX Key Location/Qualifiers
FH Domain 1..46
FT Domain /label= Intracellular_domain
FT Domain 47..72
FT Domain /label= Transmembrane_domain
FT Domain 73..285
FT Domain /label= Extracellular_domain
FT Binding-site 123..285
FT /label= TACI binding site
FT /note= "Binds with extracellular domain of TACI"
XX WO2000067034-A1.
XX 09-NOV-2000.
XX 14-APR-2000; 2000WO-US10282.
XX 30-APR-1999; 99US-0302863.
XX (IMMU) IMMUNEX CORP.
XX Goodwin RG, Din WS;
XX WPI; 2001-016005/02.
XX N-PSDB; AAD02007.
XX Use of new interactions between tumour necrosis factor receptors (TACI)
PT and TACI ligands to screen candidate molecules for determining agonist
PT and antagonist interactions which are used for treating inflammation -
XX Claim 10; Fig 2b; 46pp; English.
XX The present sequence is a human tumour necrosis factor receptor
CC (TACI)-ligand (TACI-L) protein.
CC TACI (Transmembrane activator and calcium-signal modulating
CC cyclophilin ligand (CAML)-interactor) forms a complex with neutrokinine

CC alpha polypeptide (TACI-Ligand). The antagonist or agonist of
CC TACI/TACI-L complex is useful for modulating an intracellular signalling
CC cascade mediated by TACI/TACI-L complex. Antagonists of TACI/TACI-L
CC complex are used to inhibit the interaction between TACI and TACI-L for
CC therapeutic purposes to treat tumour and tumour metastasis and to combat
CC various autoimmune diseases e.g. multiple sclerosis and diabetes, as
CC well as other disorders, such as viral infection, rheumatoid arthritis,
CC graft rejection, and immunoglobulin (Ig) E-mediated allergic reactions
CC and inflammation. The interaction is used to study cellular processes
CC associated with tumour necrosis factor (TNF)-receptors such as immune
CC regulation, cell proliferation, cell death and inflammatory responses.
CC The interaction between the extracellular region of TACI and TACI-L can
CC be used to further develop understanding of which cell types TACI-L
CC acts upon.
xx

SQ	Sequence	285 AA;
Query Match	100.0%;	Score 1451; DB 22; Length 285;
Best Local Similarity	100.0%;	Pred. No. 4.4e-145;
Matches 285;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	MDDSTEREQSLTCLKKREMKLKCVCVSLPKESPVRSSKDGKLLAATLLALLSCC 60
Db	1	MDDSTEREQSLTCLKKREMKLKCVCVSLPKESPVRSSKDGKLLAATLLALLSCC 60
QY	61	LTVVSFYQVAALQGLASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
Db	61	LTVVSFYQVAALQGLASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPAP 120
QY	121	EGNSSNSNRKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPWLLSFKRGSALEE 180
Db	121	EGNSSNSNRKRAVQGPETVTQDCLQIADSETPTIQKSYTFVPWLLSFKRGSALEE 180
QY	181	KENKILYKETGYFFIYGQVLYTDKTYAMGHLIQKKVHVFGDELSLVTLPFCIQNMPETL 240
Db	181	KENKILYKETGYFFIYGQVLYTDKTYAMGHLIQKKVHVFGDELSLVTLPFCIQNMPETL 240
QY	241	PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDTFFGALKIL 285
Db	241	PNNSCYSAGIAKLEEGDELQLAIPRENAQISLDGDTFFGALKIL 285

Search completed: August 28, 2003, 18:03:25
Job time : 88 secs

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	110.5	7.6	235	2	JU0029	tumor necrosis fac	
2	109.5	7.5	233	1	S11688	tumor necrosis fac	
3	109.5	7.5	235	1	QWMSN	tumor necrosis fac	
4	108	7.4	233	1	S24642	tumor necrosis fac	
5	107.5	7.4	235	2	IS4490	tumor necrosis fac	
6	107	7.4	232	2	S06192	tumor necrosis fac	
7	107	7.4	232	1	S12606	tumor necrosis fac	
8	102.5	7.1	234	1	JH0529	tumor necrosis fac	
9	100.5	6.9	205	1	QWHDJ	tumor necrosis fac	
10	98.5	6.8	233	1	QWHDJ	lymphotoxin alpha	
11	98	6.8	234	1	A25451	tumor necrosis fac	
12	97.5	6.7	184	2	A82993	tumor necrosis fac	
13	97.5	6.7	281	2	I38707	hypothetical prote	
14	94.5	6.5	347	2	A75537	Fas ligand - human	
15	93.5	6.4	651	1	RGBYD2	hypothetical prote	
16	93	6.4	596	2	B96834	translation regula	
17	92.5	6.4	185	2	S52715	hypothetical prote	
18	90.5	6.2	203	1	S17289	tumor necrosis fac	
19	89.5	6.2	233	1	S22052	tumor necrosis fac	
20	89.5	6.2	234	1	J01344	tumor necrosis fac	
21	88.5	6.1	631	2	A35565	tumor necrosis fac	
22	87.5	6.0	919	2	F83257	hypothetical prote	
23	87.5	6.0	993	2	A38437	hypothetical prote	
24	87	6.0	273	2	T49495	probable homeotic	
25	86.5	6.0	1229	2	D85023	probable phosphom	
26	86.5	6.0	1229	2	T52319	p-glycoprotein-lik	
27	85.5	5.9	204	1	S24641	lymphotoxin - bovi	
28	85.5	5.9	351	2	S40840	hypothetical 39.3K	
29	85.5	5.9	358	1	W2WL51	E2 protein - human	

Db 82 -----SSQNSDDKPVAVHVAHQAEQLEWLSQRANALLANG-----M 120
 QY 179 EEKENKILVKTGFFFIYGVLYTDK-----TYAMGHILQIRKKVHVFGDELSLTLFR--C 232
 Db 121 DLKDNQVVPADGLYLIYSQVLFKQGCQPDVLLTHVSRFAIS-YQEKVSLLSAISKSPC 179
 QY 233 IQNMPETLP-----NNSCSAGIAKLEGEDELQLAIPRENAQISLDG--DVT-----PFGA 281
 Db 180 PKDTPGAEALKPWEPMYLGGVQFQLEKGDLL-----SAFVNLPKYLDITQESQGVFVG 232
 QY 282 LKL 284
 Db 233 IAL 235

RESULT 2
 S11688
 tumor necrosis factor alpha precursor - cat
 C:Species: Felis silvestris catus (domestic cat)
 C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Feb-2000
 R:McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A.
 Nucleic Acids Res. 18, 5563, 1990
 A:Title: Gene sequence of feline tumor necrosis factor alpha.
 A:Reference number: S11688; MUID:91016860; PMID:2216740
 A:Accession: S11688
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-233 <MCWG>
 A:Cross-references: EMBL:X54000; NID:g1084; PIDN:CAA37948.1; PID:g295777
 C:Genetics: 62/3; 78/1; 94/1
 C:Superfamily: tumor necrosis factor
 C:Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
 F:19,20/Binding site: myristate (Lys) (covalent) #status predicted
 F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F:145-177/Disulfide bonds: #status predicted

Query Match 7.5%; Score 109.5; DB 2; Length 233;
 Best Local Similarity 22.7%; Pred. No. 0.068;
 Matches 55; Conservative 35; Mismatches 95; Indels 57; Gaps 10;
 QY 60 CLTVVSFQVVALQGLDASLRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFEPPA 119
 Db 32 CLSLFSLVAGATYLCFLHFGVIGPQRELP-----HGLQLINLP 74
 QY 120 PGEGNSSQNRNK-----RAVQGPETVTQDCLQIADSETPTIQKSYTFVFWLLSFKRGS 176
 Db 75 QTLRSSRTPSPDKPVAVHVAQNP-----AEGQLQLSRANALLANG----- 116
 QY 177 ALBEKENKILVKTGFFFIYGVLYTDKTYAMGHILQIRKKVHVFG-----DELSLTLFR- 231
 Db 117 -VELTDNQLKVPDGLYLIYSQVLFKQGCQPDVLLTHVSRFAISYQEKVSLLSAISKSPC 175
 QY 232 -CIGNMPETLPNNSCYS-----AGIAKLEGEDELQLAIPRENAQISLDG--DVT-----PFGA 281
 Db 176 PQRETPEGAELKPWEPMYLGGVQFQLEKGDRLSTEI---NLPAYLDPAESQGVYFGLI 231
 QY 283 KL 284
 Db 232 AL 233

RESULT 3
 QMNSN
 tumor necrosis factor alpha precursor - mouse
 N:Alternate names: cachectin; TNF alpha
 C:Species: Mus musculus (house mouse)
 C>Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 04-Feb-2000
 C:Accession: A22908; S03791; A23127; A34251; I59058; A36696
 R:Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
 DNA 7, 193-201, 1988
 A:Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis

A:Reference number: A22908; MUID:88224564; PMID:2836146
 A:Accession: A22908
 A:Molecule type: DNA
 A:Residues: 1-235 <SHI>
 A:Cross-references: GB:M20155
 R:Shakhov, A.N.; Nedospasov, S.A.
 Bioorg. Khim. 13, 701-705, 1987
 A:Title: Molecular cloning of the genes coding for tumor necrosis factors: complete n
 A:Reference number: S03791; MUID:87298639; PMID:3040015
 A:Accession: S03791
 A:Molecule type: DNA
 A:Residues: 1-235 <SHA>
 A:Cross-references: GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:g202087
 A>Note: article in Russian with English abstract
 R:Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
 Nucleic Acids Res. 15, 9083-9084, 1987
 A:Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor
 A:Reference number: A93679; MUID:88067722; PMID:3684584
 A:Accession: A27303
 A:Molecule type: DNA
 A:Residues: 1-235 <SEM>
 A:Cross-references: GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID:g54832
 R:Pennica, D.; Hayflick, J.S.; Bringham, T.S.; Palladino, M.A.; Goeddel, D.V.
 Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985
 A:Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necr
 A:Reference number: A25164; MUID:85298296; PMID:3898078
 A:Accession: A25164
 A:Molecule type: mRNA
 A:Residues: 1-235 <PEN>
 A:Cross-references: GB:M11731; NID:g202084; PIDN:AAA40458.1; PID:g202085
 R:Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashim
 Nucleic Acids Res. 13, 4417-4429, 1985
 A:Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic ex
 A:Reference number: A23127; MUID:85242112; PMID:2989794
 A:Accession: A23127
 A:Molecule type: mRNA
 A:Residues: 1-235 <FRA>
 A:Cross-references: GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g54845
 R:Cseh, K.; Beutler, B.
 J. Biol. Chem. 264, 16256-16260, 1989
 A:Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide resul
 A:Reference number: A34251; MUID:89380231; PMID:2777790
 A:Accession: A34251
 A:Molecule type: protein
 A:Residues: 70-87 <CSE>
 R:Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.
 Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
 A:Title: Identification of a common nucleotide sequence in the 3'-untranslated region
 A:Reference number: I59058; MUID:86149365; PMID:2419912
 A:Accession: I59058
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-230, 'R', 232-235 <RES>
 A:Cross-references: GB:M13049; NID:g202082; PIDN:AAA40457.1; PID:g202083
 R:Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.
 Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990
 A:Title: Characterization of high molecular weight glycosylated forms of murine tumor
 A:Reference number: A36696; MUID:91097531; PMID:2268312
 A:Accession: A36696
 A:Molecule type: protein
 A:Residues: 80-85, 'X', 87-99 <SHE>
 C:Genetics:
 A:Introns: 62/3; 81/1; 97/1
 A>Note: the first intron occurs in the 5'-untranslated region
 C:Superfamily: tumor necrosis factor
 C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m
 F:80-235/Product: tumor necrosis factor #status experimental <WAT>
 F:20/Binding site: myristate (Lys) (covalent) #status predicted
 F:84/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F:86/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:148-179/Disulfide bonds: #status predicted

Query Match 7.5%; Score 109.5; DB 1; Length 235;

C; Keywords: cytokine; cytotoxin; glycoprotein; IL-42/Binding site; carbohydrate (Ser) (covalent)

C; Keywords: cytokine; cytotoxin; glycoprotein; IL-42/Binding site; carbohydrate (Ser) (covalent)

F:106-138/Disulfide bonds: #status predicted

Query Match 7.4%; Score 107; DB 2; Length 193;
Best Local Similarity 23.4%; Pred. No. 0.089;
Matches 50: Conservative 36; Mismatches 92; Indels

[illegible]

RESULT 7

tumor necrosis factor alpha precursor - pig
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 10-Sep-1999 #sequence.revision 10-Sep-1999 #text_change 04-Feb-2000
 C:Accession: S12606; S17290; S18965; I46659
 R:Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
 Nucleic Acids Res. 18, 5564, 1990
 A:Title: Gene sequence of porcine tumor necrosis factor alpha.
 A:Reference number: S12606; MUID:91016861; PMID:2216741
 A:Accession: S12606
 A:Molecule type: DNA
 A:Residues: 1-232 <DRE>
 A:Cross-references: EMBL:X54001; NID:g2135; PIDN:CAA37949.1; PID:g2136
 R:Kumert, P.; Wuethrich, C.; Peterhans, E.; Paulli, U.
 Gene 102, 171-178, 1991
 A:Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative anal
 A:Reference number: S17289; MUID:91340150; PMID:1874444
 A:Accession: S17290
 A:Molecule type: DNA
 A:Residues: 1-232 <KUH>
 A:Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134
 A:Note: the authors translated the codon GAG for residue 202 as Gly
 R:Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.
 Submitted to the EMBL Data Library, January 1991
 A:Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis fa
 A:Reference number: S18965
 A:Accession: S18965
 A:Molecule type: mRNA
 A:Residues: 1-232 <CHO>
 A:Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138
 R:Paulli, U.; Reutler, B.; Peterhans, E.
 Gene 81, 195-191, 1989
 A:Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reaction
 A:Reference number: I46659; MUID:90034181; PMID:2478420
 A:Accession: I46659
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 44-232 <PAU>
 A:Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695
 C:Genetics:
 A:Introns: 62/3; 78/1; 93/1
 C:Superfamily: tumor necrosis factor
 C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myri
 F:1-77/Domain: propeptide #status predicted <PRO>
 F:78-232/Product: tumor necrosis factor alpha #status predicted <MAT>
 F:19,20/Binding site: myristate (Lys) (covalent) #status predicted
 F:81/Binding site: carbohydrate (Ser) (covalent) #status predicted
 F:144-176/Disulfide bonds: #status predicted

Query Match	7.4%;	Score 107;	DB 1;	Length 232;
Best Local Similarity	22.0%;	Pred. No. 0.11;		

[illegible]

RESULT 8

tumor necrosis factor alpha precursor - sheep
N:Alternate names: cachectin; TNF alpha
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
A:Accession: JH0529; S48118; S13114; S20661
R:Green, I.R.; Sargan, D.R.
Gene 109, 203-210, 1991
A:Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems w
A:Reference number: JH0529; MUID:92112044; PMID:1765267
A:Accession: JH0529
A:Molecule type: mRNA
A:Residues: 1-234 <GRE>
A:Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406
A:Experimental source: alveolar macrophage
R:Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.
Immunol. Cell Biol. 69, 273-283, 1991
A:Title: Molecular cloning, expression and characterization of ovine TNF-alpha.
A:Reference number: S48118; MUID:92155784; PMID:1786996
A:Accession: S48118
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-234 <N>
A:Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807
R:Young, A.J.; Hay, J.B.; Chan, J.Y.C.
Nucleic Acids Res. 18, 6723, 1990
A:Title: Primary structure of ovine tumor necrosis factor alpha cDNA.
A:Reference number: S13114; MUID:91067496; PMID:2251151
A:Accession: S13114
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-62,64-234 <YOU>
A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404
A:Note: comparison with the introns of homologous sequences suggest that this is prob
C:Superfamily: tumor necrosis factor
C:Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lym
F:1-77/Domain: propeptide #status predicted <PRO>
F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F:20/Binding site: myristate (lys) (covalent) #status predicted
F:82/Binding site: carboxylate (Ser) (covalent) #status predicted
F:96/Binding site: carboxylate (Asn) (covalent) #status predicted
F:146-178/Disulfide bonds: #status predicted

Query Match 7.1%; Score 102.5; DB 1; Length 234;
Best Local Similarity 22.5%; Pred. No. 0.27;
Matches 56; Conservative 41; Mismatches 87; Indels 65; Gaps 12;

```
QY 58 SC-CLTVVSVQVAALODGLASRAELQGHAEKLPAGAGAPKAGLEAPAVTAGLKIFE 116
Db 29 SCWCLSLFSLVAGATTLFCLLHFGVIGPQRE-----EQSP---AGPSFNR 72
QY 117 PPAPGEGNSSNSNRKAVQGPETVTDCLQLIADSETPTIOKGYTFVFWLLSKRGS 176
Db 73 PLVOTLRSSQASNNKPA-----HVVANISAPGQLRWGSDSYANALMA-----N 116
QY 177 ALEKENKILVKETGYFIYQGVLY-----TDKTYAMGHILQKVKHVFGEDELSTLPLR 231
Db 117 GVELKQNLVPTDGLYLIYSQVLFRCGHGCPSPFLTFHTISRIANS-YQTKVNILSAIK 175
QY 232 --CIGNMPETLPN-----NSCVSAGIAKLEGEDELQAIAPRENAQISL-----DGD 275
Db 176 SPCHR---ETLEGAEPWPEIYQGGVQLEKGRDL-----SAEINLPEYLDVAESG 225
QY 276 VTFEGALKL 284
Db 226 QVYEGITAL 234

RESULT 9
QWHUX
Lymphotoxin alpha precursor - human
N:Alternate names: lymphotoxin A; TNF beta; tumor necrosis factor beta (TNF beta)
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 07-Jul-1995 #text_change 16-Jun-2000
A:Accession: A92755; S36154; I54482; B32877; A91906; A61478; S26951; A01645; A23
R:Nedwin, G.E.; Jarrett-Nedwin, J.; Smith, D.H.; Naylor, S.L.; Sakaguchi, A.Y.; Goeddel,
J. Cell. Biochem. 29, 171-181, 1985
A:Title: Structure and chromosomal localization of the human lymphotoxin gene.
A:Reference number: A92755; MUID:86086150; PMID:3001109
A:Accession: A92755
A:Molecule type: DNA
R:Residues: 1-59, 'N', 61-205 <NED>
R:Iris, F.J.M.; Bouqueloret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka
Nature Genet. 3, 137-145, 1993
A:Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
A:Reference number: S36152; MUID:93272029; PMID:8499947
A:Accession: S36154
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
R:Residues: 1-12, 'R', 14-205 <IRI>
A:CROSS-references: EMBL:Z15026; NID:g37211; PIDN:CAA78746.1; PID:g37213
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R:Abraham, L.J.; Du, D.C.; Zahedi, K.; Dawkins, R.L.; Whitehead, A.S.
Immunogenetics 33, 50-53, 1991
A:Title: Haplotypic polymorphisms of the TNFB gene.
A:Reference number: I54482; MUID:91139175; PMID:1671667
A:Accession: I54482
A>Status: translation not shown; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
R:Residues: 1-124, 'P', 126-205 <RES>
A:CROSS-references: GB:M55913; NID:g339742; PIDN:AAB59455.1; PID:g339743
A:Experimental source: ancestral haplotype 57.1
A:Note: 59-Asn was also found (ancestral haplotype 8.1)
R:Gray, P.W.; Aggarwal, B.B.; Benton, C.V.; Bringman, T.S.; Henzel, W.J.; Jarrett, J.A.;
Nature 312, 721-724, 1984
A:Title: Cloning and expression of cDNA for human lymphotoxin, a lymphokine with tumour
A:Reference number: A93350; MUID:85086243; PMID:6334807
A:Accession: A93350
A:Molecule type: mRNA
R:Residues: 1-205 <GRA>
A:CROSS-references: GB:X01393; NID:g34444; PIDN:CAA25649.1; PID:g34445
A:Experimental source: lymphoblastoid cell line RPMI-1788
R:Goeddel, D.V.; Aggarwal, B.B.; Gray, P.W.; Leung, D.W.; Nedwin, G.E.; Palladino, M.A.;
Cold Spring Harb. Symp. Quant. Biol. 51, 597-609, 1986
A:Title: Tumor necrosis factors: gene structure and biological activities.
A:Reference number: A32877; MUID:87217059; PMID:3472740
A:Accession: B32877
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
R:Residues: 35-205 <GOE>
```

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R; Kobayashi, Y.; Miyamoto, D.; Asada, M.; Obinata, M.; Osawa, T.
J. Biochem. 100, 727-733, 1986
A:Title: Cloning and expression of human lymphotoxin mRNA derived from a human T cell
A:Reference number: A91906; MUID:87057135; PMID:3536896
A:Accession: A91906
A:Molecule type: mRNA
R:Residues: 1-59, 'N', 61-205 <KOB>
A:CROSS-references: GB:D00102; NID:g219913; PIDN:BAA00064.1; PID:g219914
A:Note: the authors translated the codon TAT for residue 156 as Thr and ACC for resid
R; Fukuda, S.; Ando, S.; Sanou, O.; Tanai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.;
Lymphokine Res. 7, 175-185, 1988
A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta
A:Reference number: A61478; MUID:88301617; PMID:2841543
A:Accession: A61478
A:Molecule type: protein
R:Residues: 56-79; 86-95, 'X', 97, 'X', 99; 119-151, 'XX', 154-162, 'X', 164, 'X', 166, 'X', 168, 'X'
FEBS Lett. 314, 85-88, 1992
R; Voigt, C.G.; Maurer-Fogy, I.; Adolff, G.R.
A:Title: Natural human tumor necrosis factor beta (lymphotoxin). Variable O-glycosyla
A:Reference number: S26951; MUID:93083656; PMID:1451807
A:Accession: S26951
A:Molecule type: protein
R:Residues: 35-59, 'N', 61-205 <VOI>
A:Note: 60-Thr was also found
R; Fukushima, K.; Watanabe, H.; Takeo, K.; Nomura, M.; Asahi, T.; Yamashita, K.
Arch. Biochem. Biophys. 304, 144-153, 1993
A:Title: N-linked sugar chain structure of recombinant human lymphotoxin produced by
A:Reference number: S34742; MUID:93311995; PMID:8323280
A:Contents: annotation
C:Comment: Secreted from mitogen-activated lymphocytes within 1-2 days after induction
while having no detrimental effect on normal cells. It can also act synergistically
C:Comment: This protein and TNF-alpha (tumor necrosis factor) are the products of dif
ical activities but are produced by different cell types and have different induction
C:Genetics:
A:Gene: GDB:UTA; LT; TNFB
A:CROSS-references: GDB:120442; OMIM:153440
A:Map position: 6p21.3-6p21.3
A:Introns: 33/3; 69/1
A:Note: the first intron occurs before the initiator codon
C:Superfamily: tumor necrosis factor
C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lymphokine; macrophage
F:1-34/Domain: signal sequence #status predicted <SIG>
F:35-205/Product: lymphotoxin #status predicted <MAT>
F:41/Binding site: carboxylate (Thr) (covalent) #status experimental
F:96/Binding site: carboxylate (Asn) (covalent) #status experimental
Query Match 6.9%; Score 100.5; DB 1; Length 205;
Best Local Similarity 23.6%; Pred. No. 0.35;
Matches 51; Conservative 20; Mismatches 84; Indels 61; Gaps 9;
QY 91 LPAGAGAPKAGLEAPAVTA-----GLKIFEPAPGEGN-SSONSRRKRAYGPPET 141
Db 29 LPGAAGLFGVGLTPSAQTARQHPKMHIAHSTLKPAAHLIGDPSKQNSLLMRA--NTDRA 86
QY 142 VTQDCLQLIADSETPTIOKGYTFVFWLLSKRGSALKEENKILVKETGYFIYQGVLY 201
Db 87 FLQDGFSL-----SNNSLVPTSGIYFYVQVVF 115
QY 202 TDKTYA---MGHLLQKRVKHVFGDELSTLVLFRICQNMPETLPN-----NSCVSAGIA 251
Db 116 SGKAYSPRKATSPSLYLAHEVOLFSQYPFHVLPLSSQKM--VYPGLQEPHLHSMVHGAA 173
QY 252 KLEEGDELQ-----AIPRENAQISLDGDVTFEGALKL 284
Db 174 QLTQGDQLSTHTDGP-----HLVLSPTSTVFFGAFAL 205

RESULT 10
QWHUN
tumor necrosis factor alpha precursor [validated] - human
N:Alternate names: cachectin; TNFA
C:Species: Homo sapiens (man)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 08-Dec-2000
```

A:Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23
 R: Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D.
 Nucleic Acids Res. 13, 6361-6373, 1985
 A:Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chro
 A:Reference number: A93585; MUID:86016093; PMID:2995927
 A:Accession: A93585
 A:Molecule type: DNA
 A:Residues: 1-233 <NED>
 A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
 R: Iris, F.J.M.; Bouquellet, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka
 Nature Genet. 3, 137-145, 1993
 A:Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
 A:Reference number: S36153; MUID:93272029; PMID:8499947
 A:Accession: S36153
 A:Molecule type: DNA
 A:Residues: 1-233 <IRI>
 A:Cross-references: EMBL:X15026; NID:g37211; PIDN:CAA78745.1; PID:g37212
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
 R: Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.
 Nature 312, 724-729, 1984
 A:Title: Human tumour necrosis factor: precursor structure, expression and homology to l
 A:Reference number: A93351; MUID:85086244; PMID:6392892
 A:Accession: A93351
 A:Molecule type: mRNA
 A:Residues: 1-233 <PEN>
 A:Cross-references: GB:X02910; GB:X02159; NID:g37209; PIDN:CAA26669.1; PID:g37210
 A:Note: this protein was isolated from the monocytic-like cell line HL-60 from a J.M.Yelc
 R: Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.;
 Science 228, 149-154, 1985
 A:Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
 A:Reference number: A44189; MUID:85142190; PMID:3856324
 A:Accession: A44189
 A:Molecule type: mRNA
 A:Residues: 1-62, 'S', '64-233 <WAN>
 A:Cross-references: GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:g339738
 R: Fukuda, S.; Ando, S.; Sanou, O.; Tani, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An
 Lymphokine Res. 7, 175-185, 1988
 A:Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
 A:Reference number: A61478; MUID:88301617; PMID:2841543
 A:Accession: B61478
 A:Molecule type: protein
 A:Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180
 R: Warneinout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,
 Eur. J. Biochem. 152, 515-522, 1985
 A:Title: Molecular cloning and expression of human tumor necrosis factor and comparison
 A:Reference number: I53311; MUID:86030296; PMID:3932069
 A:Accession: I53311
 A:Molecule type: DNA
 A:Status: translated from GB/EMBL/DBDJ
 A:Residues: 1-233 <WAB>
 A:Cross-references: GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:g339764
 A:Experimental source: U-937 cells
 R: Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
 Eur. J. Biochem. 235, 431-437, 1996
 A:Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
 A:Reference number: S62610; MUID:96202967; PMID:8631363
 A:Accession: S62610
 A:Molecule type: protein
 A:Residues: 77-99 <TAK>
 R: D'Alfonso, S.; Ricciardi, P.M.
 Immunogenetics 39, 150-154, 1994
 A:Title: A polymorphic variation in a putative regulation box of the TNFA promoter regic
 A:Reference number: I54522; MUID:94102809; PMID:7903959
 A:Accession: I54522
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-8 <DAL>
 A:Cross-references: GB:S68530; NID:G544751
 R: Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
 J. Exp. Med. 176, 1053-1062, 1992
 A:Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific lys
 A:Reference number: A59163; MUID:93018820; PMID:1402651

A:Contents: annotation; identification of myristylated lysines
 R: Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Br
 J. Biol. Chem. 260, 2345-2354, 1985
 A:Title: Human tumor necrosis factor. Production, purification, and characterization.
 A:Reference number: A92511; MUID:85130974; PMID:3671770
 A:Contents: annotation; disulfide bond
 A:Comment: Secreted from mitogen-activated macrophages within 4-24 hours after induc
 out detriment to normal cells. It can also act synergistically with interferon gamma
 A:Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes clos
 ut are produced by different cell types and have different induction kinetics.
 C:Genetics:
 A:Gene: GDB:TNF; TNFA
 A:Cross-references: GDB:120441; OMIM:191160
 A:Map position: 6p21.3-6p21.3
 A:Introns: 62/3; 78/1; 94/1
 C:Complex: homotrimer
 C:Superfamily: tumor necrosis factor
 C:Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; m
 F:1-76/Domain: propeptide status predicted <PRO>
 F:17-233/Product: tumor necrosis factor status experimental <WAT>
 F:19,20/Binding site: myristate (lys) (covalent) status experimental
 F:81/Binding site: carbohydrate (Ser) (covalent) (partial) status experimental
 F:145-177/Disulfide bonds: status experimental
 Query Match 6.88; Score 98.5; DB 1; Length 233;
 Best Local Similarity 24.28; Pred. NO. 0.6;
 Matches 44; Conservative 34; Mismatches 69; Indels 35; Gaps 9;
 Qy 135 VQPEETVTDCLQLI-----ADSETPTIQSGYTF-----VPMLLSFKRGSAL 178
 Db 55 VIGPQREFFPRDLISLPLAQAVRSRSTPSDKPVAHVANPQAEGLQWL--NRRANAL 112
 Qy 179 -----EKENKILVETGYFFIYGVLYTDK----TYA-MGLIQKVVHFGDELSLYT 228
 Db 113 LANGVELRDNLQVVPSEGLYISQVLFKQGPCSTHVLTHTRISRAVS-YOTKVNLLS 171
 Qy 229 LFR--CQNNPPTLPNNSCYS---AGIAKLEGEDELQALPENAQISLDGQVTFEGAL 282
 Db 172 AIKSPQCRETPGEAKPWEPYILGVGFQLEKGRLSAEINRPDYLDPAESQGVYFGII 231
 Qy 283 KL 284
 Db 232 AL 233
 RESULT 11
 A25451
 tumor necrosis factor alpha precursor - rabbit
 N:Alternate names: cachectin; TNF alpha
 C:Species: Oryctolagus cuniculus (domestic rabbit)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 04-Feb-2000
 C:Accession: A25454; A25451; JS0727
 R: Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi,
 DNA 5, 149-156, 1986
 A:Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for
 A:Reference number: A25454; MUID:86219711; PMID:3519137
 A:Accession: A25454
 A:Molecule type: mRNA
 A:Residues: 1-234 <ITO>
 A:Cross-references: GB:M12845; NID:gl65759; PIDN:AAA31486.1; PID:gl65760
 R: Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.
 DNA 5, 157-165, 1986
 A:Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
 A:Reference number: A25451; MUID:86219712; PMID:3519138
 A:Accession: A25451
 A:Molecule type: DNA
 A:Residues: 1-234 <IT2>
 A:Note: this sequence differs from that shown in having a Gln inserted between residu
 R: Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
 Gene 95, 215-221, 1990
 A:Title: Structural analysis of the rabbit TNF locus, containing the genes encoding T
 A:Reference number: JH0309; MUID:91065534; PMID:2249779
 A:Accession: JS0727

